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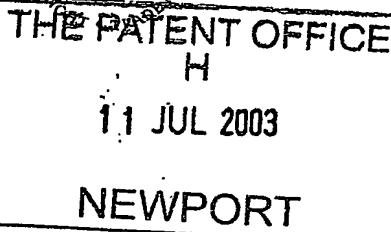
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SUBSTANCES

The present invention relates to proteinaceous particles, for example phage or ribosome particles, displaying T cell receptors (TCRs).

5

Background to the Invention

Native TCRs

As is described in, for example, WO 99/60120 TCRs mediate the recognition of specific Major Histocompatibility Complex (MHC)-peptide complexes by T cells and, 10 as such, are essential to the functioning of the cellular arm of the immune system.

Antibodies and TCRs are the only two types of molecules which recognise antigens in a specific manner, and thus the TCR is the only receptor for particular peptide antigens presented in MHC, the alien peptide often being the only sign of an abnormality 15 within a cell. T cell recognition occurs when a T-cell and an antigen presenting cell (APC) are in direct physical contact, and is initiated by ligation of antigen-specific TCRs with pMHC complexes.

The native TCR is a heterodimeric cell surface protein of the immunoglobulin 20 superfamily which is associated with invariant proteins of the CD3 complex involved in mediating signal transduction. TCRs exist in $\alpha\beta$ and $\gamma\delta$ forms, which are structurally similar but have quite distinct anatomical locations and probably 25 functions. The MHC class I and class II ligands are also immunoglobulin superfamily proteins but are specialised for antigen presentation, with a highly polymorphic peptide binding site which enables them to present a diverse array of short peptide fragments at the APC cell surface.

Two further classes of proteins are known to be capable of functioning as TCR 30 ligands. (1) CD1 antigens are MHC class I-related molecules whose genes are located on a different chromosome from the classical MHC class I and class II antigens. CD1 molecules are capable of presenting peptide and non-peptide (eg lipid, glycolipid)

moieties to T cells in a manner analogous to conventional class I and class II-MHC-pep complexes. See, for example (Barclay et al, (1997) The Leucocyte Antigen Factsbook 2nd Edition, Academic Press) and (Bauer (1997) Eur J Immunol 27 (6) 1366-1373)) (2) Bacterial superantigens are soluble toxins which are capable of binding both class II MHC molecules and a subset of TCRs. (Fraser (1989) Nature 339 221-223) Many superantigens exhibit specificity for one or two V_{beta} segments, whereas others exhibit more promiscuous binding. In any event, superantigens are capable of eliciting an enhanced immune response by virtue of their ability to stimulate subsets of T cells in a polyclonal fashion.

10

The extracellular portion of native heterodimeric $\alpha\beta$ and $\gamma\delta$ TCRs consist of two polypeptides each of which has a membrane-proximal constant domain, and a membrane-distal variable domain. Each of the constant and variable domains includes an intra-chain disulfide bond. The variable domains contain the highly polymorphic loops analogous to the complementarity determining regions (CDRs) of antibodies. CDR3 of $\alpha\beta$ TCRs interact with the peptide presented by MHC, and CDRs 1 and 2 of $\alpha\beta$ TCRs interact with the peptide and the MHC. The diversity of TCR sequences is generated via somatic rearrangement of linked variable (V), diversity (D), joining (J), and constant genes

20

Functional α and γ chain polypeptides are formed by rearranged V-J-C regions, whereas β and δ chains consist of V-D-J-C regions. The extracellular constant domain has a membrane proximal region and an immunoglobulin region. There are single α and δ chain constant domains, known as TRAC and TRDC respectively. The β chain constant domain is composed of one of two different β constant domains, known as TRBC1 and TRBC2 (IMGT nomenclature). There are four amino acid changes between these β constant domains, three of which are within the domains used to produce the single-chain TCRs displayed on phage particles of the present invention. These changes are all within exon 1 of TRBC1 and TRBC2: N₄K₅>K₄N₅ and F₃₇>Y

25

(IMGT numbering, differences TRBC1->TRBC2), the final amino acid change

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between the two TCR β chain constant regions being in exon 3 of TRBC1 and TRBC2: V₁->E. The constant γ domain is composed of one of either TRGC1, TRGC2(2x) or TRGC2(3x). The two TRGC2 constant domains differ only in the number of copies of the amino acids encoded by exon 2 of this gene that are present.

5

The extent of each of the TCR extracellular domains is somewhat variable. However, a person skilled in the art can readily determine the position of the domain boundaries using a reference such as The T Cell Receptor Facts Book, Lefranc & Lefranc, Publ. Academic Press 2001.

10

Recombinant TCRs

The production of recombinant TCRs is beneficial as these provide soluble TCR analogues suitable for the following purposes:

15

- Studying the TCR / ligand interactions (e.g. pMHC for $\alpha\beta$ TCRs)
- Screening for inhibitors of TCR-associated interactions
- Providing the basis for potential therapeutics

20

A number of constructs have been devised to date for the production of recombinant TCRs. These constructs fall into two broad classes, single-chain TCRs and dimeric TCRs, the literature relevant to these constructs is summarised below.

Single-chain TCRs (scTCRs) are artificial constructs consisting of a single amino acid strand, which like native heterodimeric TCRs bind to MHC-peptide complexes.

25

Unfortunately, attempts to produce functional alpha/beta analogue scTCRs by simply linking the alpha and beta chains such that both are expressed in a single open reading frame have been unsuccessful, presumably because of the natural instability of the alpha-beta soluble domain pairing.

30

Accordingly, special techniques using various truncations of either or both of the alpha and beta chains have been necessary for the production of scTCRs. These formats appear to be applicable only to a very limited range of scTCR sequences. Soo Hoo *et*

al (1992) PNAS. **89** (10): 4759-63 report the expression of a mouse TCR in single chain format from the 2C T cell clone using a truncated beta and alpha chain linked with a 25 amino acid linker and bacterial periplasmic expression (see also Schodin *et al* (1996) Mol. Immunol. **33** (9): 819-29). This design also forms the basis of the m6 5 single-chain TCR reported by Holler *et al* (2000) PNAS. **97** (10): 5387-92 which is derived from the 2C scTCR and binds to the same H2-Ld-restricted alloepitope. Shusta *et al* (2000) Nature Biotechnology **18**: 754-759 and US 6,423,538 report using a murine single-chain 2C TCR constructs in yeast display experiments, which produced mutated TCRs with, enhanced thermal stability and solubility. This 10 report also demonstrated the ability of these displayed 2C TCRs to selectively bind cells expressing their cognate pMHC. Khandekar *et al* (1997) J. Biol. Chem. **272** (51): 32190-7 report a similar design for the murine D10 TCR, although this scTCR was fused to MBP and expressed in bacterial cytoplasm (see also Hare *et al* (1999) Nat. Struct. Biol. **6** (6): 574-81). Hilyard *et al* (1994) PNAS. **91** (19): 9057-61 report a 15 human scTCR specific for influenza matrix protein-HLA-A2, using a V α -linker-V β design and expressed in bacterial periplasm.

Chung *et al* (1994) PNAS. **91** (26) 12654-8 report the production of a human scTCR using a V α -linker-V β -C β design and expression on the surface of a mammalian cell 20 line. This report does not include any reference to peptide-HLA specific binding of the scTCR. Plaksin *et al* (1997) J. Immunol. **158** (5): 2218-27 report a similar V α -linker-V β -C β design for producing a murine scTCR specific for an HIV gp120-H-2D^d epitope. This scTCR is expressed as bacterial inclusion bodies and refolded *in vitro*.

25 A number of papers describe the production of TCR heterodimers which include the native disulphide bridge which connects the respective subunits (Garboczi, *et al.*, (1996), Nature **384**(6605): 134-41; Garboczi, *et al.*, (1996), J Immunol **157**(12): 5403-10; Chang *et al.*, (1994), PNAS USA **91**: 11408-11412; Davodeau *et al.*, (1993), J. Biol. Chem. **268**(21): 15455-15460; Golden *et al.*, (1997), J. Imm. Meth. **206**: 163-30 169, US Patent No. 6080840).—However, although such TCRs can be recognised by

TCR-specific antibodies, none were shown to recognise its native ligand at anything other than relatively high concentrations and/or were not stable.

5. In WO 99/60120, a soluble TCR is described which is correctly folded so that it is capable of recognising its native ligand, is stable over a period of time, and can be produced in reasonable quantities. This TCR comprises a TCR α or γ chain extracellular domain dimerised to a TCR β or δ chain extracellular domain respectively, by means of a pair of C-terminal dimerisation peptides, such as leucine zippers. This strategy of producing TCRs is generally applicable to all TCRs.

10

Reiter *et al*, *Immunity*, 1995, **2**:281-287, details the construction of a soluble molecule comprising disulphide-stabilised TCR α and β variable domains, one of which is linked to a truncated form of *Pseudomonas* exotoxin (PE38). One of the stated reasons for producing this molecule was to overcome the inherent instability of single-chain TCRs. The position of the novel disulphide bond in the TCR variable domains was identified via homology with the variable domains of antibodies, into which these have previously been introduced (for example see Brinkmann, *et al.* (1993), *Proc. Natl. Acad. Sci. USA* **90**: 7538-7542, and Reiter, *et al.* (1994) *Biochemistry* **33**: 5451-5459). However, as there is no such homology between antibody and TCR constant domains, such a technique could not be employed to identify appropriate sites for new inter-chain disulphide bonds between TCR constant domains.

25 As mentioned above Shusta *et al* (2000) *Nature Biotechnology* **18**: 754-759 report using single-chain 2 C TCR constructs in yeast display experiments. The principle of displaying scTCRs on phage particles has previously been discussed. For example, WO 99/19129 details the production of scTCRs, and summarise a potential method for the production of phage particles displaying scTCRs of the $V\alpha$ -Linker- $V\beta$ C β format. However, this application contains no exemplification demonstrating the production of said phage particles displaying TCR. The application does however refer to a co-pending application:

30

"The construction of DNA vectors including a DNA segment encoding a sc-TCR molecules fused to a bacteriophage coat protein (gene II or gene VIII) have been described in said pending U.S. application No. 08/813,781."

5 Furthermore, this application relies on the ability of anti-TCR antibodies or super-antigen MHC complexes to recognise the soluble, non-phage displayed, scTCRs produced to verify their correct conformation. Therefore, true peptide-MHC binding specificity of the scTCRs, in any format, is not conclusively demonstrated.

10 *Screening Use*

A number of important cellular interactions and cell responses, including the TCR-mediated immune synapse, are controlled by contacts made between cell surface receptors and ligands presented on the surfaces of other cells. These types of specific molecular contacts are of crucial importance to the correct biochemical regulation in 15 the human body and are therefore being studied intensely. In many cases, the objective of such studies is to devise a means of modulating cellular responses in order to prevent or combat disease.

20 Therefore, methods with which to identify compounds that bind with some degree of specificity to human receptor or ligand molecules are important as leads for the discovery and development of new disease therapeutics. In particular, compounds that interfere with certain receptor-ligand interactions have immediate potential as therapeutic agents or carriers.

25 Advances in combinatorial chemistry, enabling relatively easy and cost-efficient production of very large compound libraries have increased the scope for compound testing enormously. Now the limitations of screening programmes most often reside in the nature of the assays that can be employed, the production of suitable receptor and ligand molecules and how well these assays can be adapted to high throughput screening methods.

Display Methods

It is often desirable to present a given peptide or polypeptide on the surface of a proteinaceous particle. Such particles may serve as purification aids for the peptide or polypeptide (since the particles carrying the peptide or polypeptide may be separated from unwanted contaminants by sedimentation or other methods). They may also serve as particulate vaccines, the immune response to the surface displayed peptide or polypeptide being stimulated by the particulate presentation. Protein p24 of the yeast retrotransposon, and the hepatitis B surface coat protein are examples of proteins which self assemble into particles. Fusion of the peptide or polypeptide of interest to these particle-forming proteins is a recognised way of presenting the peptide or polypeptide on the surface of the resultant particles.

However, particle display methods have primarily been used to identify proteins with desirable properties such as enhanced expression yields, binding and/or stability characteristics. These methods involve creating a diverse pool or 'library' of proteins or polypeptides expressed on the surface of proteinaceous particles. These particles have two key features, firstly each particle presents a single variant protein or polypeptide, and secondly the genetic material encoding the expressed protein or polypeptide is associated with that of the particle. This library is then subjected to one or more rounds of selection. For example, this may consist of contacting a ligand with a particle-display library of mutated receptors and identifying which mutated receptors bind the ligand with the highest affinity. Once the selection process has been completed the receptor or receptors with the desired properties can be isolated, and their genetic material can be amplified in order to allow the receptors to be sequenced.

25

These display methods fall into two broad categories, *in-vitro* and *in-vivo* display.

All *in-vivo* display methods rely on a step in which the library, usually encoded in or with the genetic nucleic acid of a replicable particle such as a plasmid or phage replicon is transformed into cells to allow expression of the proteins or polypeptides. (Plückthun (2001) *Adv Protein Chem* 55 367-403). There are a number of

replicon/host systems that have proved suitable for *in-vivo* display of protein or polypeptides. These include the following

Phage / bacterial cells

5 plasmid / CHO cells

Vectors based on the yeast 2 μ m plasmid / yeast cells

baculovirus / insect cells

plasmid / bacterial cells

10

In-vivo display methods include cell-surface display methods in which a plasmid is introduced into the host cell encoding a fusion protein consisting of the protein or polypeptide of interest fused to a cell surface protein or polypeptide. The expression of this fusion protein leads to the protein or polypeptide of interest being displayed on the surface of the cell. The cells displaying these proteins or polypeptides of interest can then be subjected to a selection process such as FACS and the plasmids obtained from the selected cell or cells can be isolated and sequenced. Cell surface display systems have been devised for mammalian cells (Higuschi (1997) J Immunol. Methods 202 193-204), yeast cells (Shusta (1999) J Mol Biol 292 949-956) and bacterial cells (Sameulson (2002) J. Biotechnol 96 (2) 129-154).

Numerous reviews of the various in-vivo display techniques have been published. For example, (Hudson (2002) Expert Opin Biol Ther (2001) 1 (5) 845-55) and (Schmitz (2000) 21 (Supp A) S106-S112).

25

In-vitro display methods are based on the use of ribosomes to translate libraries of mRNA into a diverse array of protein or polypeptide variants. The linkage between the proteins or polypeptides formed and the mRNA encoding these molecules is maintained by one of two methods. Conventional ribosome display utilises mRNA sequences that encode a short (typically 40-100 amino acid) linker sequence and the protein or polypeptide to be displayed. The linker sequence allow the displayed

protein or polypeptide sufficient space to re-fold without being sterically hindered by the ribosome. The mRNA sequence lacks a 'stop' codon, this ensures that the expressed protein or polypeptide and the RNA remain attached to the ribosome particle. The related mRNA display method is based on the preparation of mRNA sequences encoding the protein or polypeptide of interest and DNA linkers carrying a puromycin moiety. As soon as the ribosome reaches the mRNA/DNA junction translation is stalled and the puromycin forms a covalent linkage to the ribosome. For a recent review of these two related *in-vitro* display methods see (Amstutz (2001) Curr Opin Biotechnol 12 400-405).

Particularly preferred is the phage display technique which is based on the ability of bacteriophage particles to express a heterologous peptide or polypeptide fused to their surface proteins. (Smith (1985) Science 217 1315-1317). The procedure is quite general, and well understood in the art for the display of polypeptide monomers. However, in the case of polypeptides that in their native form associate as dimers, only the phage display of antibodies appears to have been thoroughly investigated.

For monomeric polypeptide display there are two main procedures:

Firstly (Method A) by inserting into a vector (phagemid) DNA encoding the heterologous peptide or polypeptide fused to the DNA encoding a bacteriophage coat protein. The expression of phage particles displaying the heterologous peptide or polypeptide is then carried out by transfecting bacterial cells with the phagemid, and then infecting the transformed cells with a 'helper phage'. The helper phage acts as a source of the phage proteins not encoded by the phagemid required to produce a functional phage particle.

Secondly (Method B), by inserting DNA encoding the heterologous peptide or polypeptide into a complete phage genome fused to the DNA encoding a bacteriophage coat protein. The expression of phage particles displaying the heterologous peptide or polypeptide is then carried out by infecting bacterial cells with the phage genome. This method has the advantage of the first method of being a

'single-step' process. However, the size of the heterologous DNA sequence that can be successfully packaged into the resulting phage particles is reduced. M13, T7 and Lambda are examples of suitable phages for this method.

5 A variation on (Method B) involves adding a DNA sequence encoding a nucleotide binding domain to the DNA in the phage genome encoding the heterologous peptide to be displayed, and further adding the corresponding nucleotide binding site to the phage genome. This causes the heterologous peptide to become directly attached to the phage genome. This peptide/genome complex is then packaged
10 into a phage particle which displays the heterologous peptide. This method is fully described in WO 99/11785.

15 The phage particles can then be recovered and used to study the binding characteristics of the heterologous peptide or polypeptide. Once isolated, phagemid or phage DNA can be recovered from the peptide- or polypeptide-displaying phage particle, and this DNA can be replicated via PCR. The PCR product can be used to sequence the heterologous peptide or polypeptide displayed by a given phage particle.

20 The phage display of single-chain antibodies and fragments thereof, has become a routine means of studying the binding characteristics of these polypeptides. There are numerous books available that review phage display techniques and the biology of the bacteriophage. (See, for example, Phage Display – A Laboratory Manual, Barbas *et al.*, (2001) Cold Spring Harbour Laboratory Press).

25 A third phage display method (Method C) relies on the fact that heterologous polypeptides having a cysteine residue at a desired location can be expressed in a soluble form by a phagemid or phage genome, and caused to associate with a modified phage surface protein also having a cysteine residue at a surface exposed position, via the formation of a disulphide linkage between the two cysteines. WO 01/05950 details
30 ~~the use of this alternative linkage method for the expression of single-chain antibody-derived peptides.~~

Brief Description of the Invention

Native TCR's are heterodimers which have lengthy transmembrane domains which are essential to maintain their stability as functional dimers. As discussed above, TCRs are useful for research and therapeutic purposes in their soluble forms so display of the insoluble native form has little utility. On the other hand, soluble stable forms of TCRs have proved difficult to design, and since most display methods appear to have been described only for monomeric peptides and polypeptides, display methods suitable for soluble dimeric TCRs have not been investigated. Furthermore, since the functionality of the displayed TCR depends on proper association of the variable regions of the TCR dimer, successful display of a functional dimeric TCR is not trivial.

WO 99/18129 contains the statement: "DNA constructs encoding the sc-TCR fusion proteins can be used to make a bacteriophage display library in accordance with methods described in pending U.S. application Serial No. 08/813.781 filed on March 15 7, 1997, the disclosure of which is incorporated herein by reference.", but no actual description of such display is included in this application. However, The inventors of this application published a paper (Weidanz (1998) J Immunol Methods 221 59-76) that demonstrates the display of two murine scTCRs on phage particles.

WO 01/62908 discloses methods for the phage display of scTCRs and scTCR/ Ig fusion proteins. However, the functionality (specific pMHC binding) of the constructs disclosed was not assessed.

Finally, a retrovirus-mediated method for the display of diverse TCR libraries on the surface of immature T cells has been demonstrated for a murine TCR. The library of mutated TCRs displayed on the surface of the immature T cells was screened by flow cytometry using pMHC tetramers, and this lead to the identification TCR variants that were either specific for the cognate pMHC, or a variant thereof. (Helmut *et al.*, (2000)

PNAS 97 (26) 14578-14583)

This invention is based in part on the finding that single chain and dimeric TCRs can be expressed as surface fusions to proteinaceous particles, and makes available proteinaceous particles displaying alpha/beta-analogue and gamma/delta-analogue scTCR and dTCR constructs. The proteinaceous particles on which the TCRs are displayed include self-aggregating particle-forming proteins, phage, virus-derived and ribosome particles. Such proteinaceous particle-displayed TCRs are useful for purification and screening purposes, particularly as a diverse library of particle displayed TCRs for biopanning to identify TCRs with desirable characteristics such as strong affinity for the target MHC-peptide complex. In the latter connection, particle-displayed scTCRs may be useful for identification of the desired TCR, but that information may be better applied to the construction of analogous dimeric TCRs for ultimate use in therapy.

Detailed Description of the Invention

15 The present invention provides a proteinaceous particle displaying on its surface a T-cell receptor(TCR), characterised in that

20 (i) the proteinaceous particle is a ribosome and the TCR is a single chain TCR (scTCR) polypeptide, or

(ii) the proteinaceous particle is a phage particle or a cell surface protein or polypeptide and the TCR is a human scTCR or a human dimeric T-cell receptor (dTCR) polypeptide pair, or

25 (iii) the proteinaceous particle is a phage particle or a cell surface protein or polypeptide and the TCR is a non-human dTCR polypeptide pair, or

(iv) the proteinaceous particle is a phage particle or a cell surface protein or polypeptide and the TCR is a scTCR polypeptide comprising TCR amino acid sequences corresponding to extracellular constant and variable region sequences present in native TCR chains and a linker sequence, the

latter linking a variable region sequence corresponding to that of one chain of a native TCR to a constant region sequence corresponding to a constant region sequence of another native TCR chain, and a disulfide bond which has no equivalent in native T cell receptors links residues of the constant region sequences.

In a preferred embodiment, the invention provides a proteinaceous particle displaying on its surface a dimeric T-cell receptor (dTCR) polypeptide pair, or a single chain T-cell receptor (scTCR) polypeptide wherein

the dTCR polypeptide pair is constituted by TCR amino acid sequences corresponding to extracellular constant and variable region sequences present in native TCR chains, and the scTCR is constituted by TCR amino acid sequences corresponding to extracellular constant and variable region sequences present in native TCR chains and a linker sequence, the latter linking a variable region sequence corresponding to that of one chain of a native TCR to a constant region sequence corresponding to a constant region sequence of another native TCR chain;

the variable region sequences of the dTCR polypeptide pair or scTCR polypeptide are mutually orientated substantially as in native TCRs; and

in the case of the scTCR polypeptide a disulfide bond which has no equivalent in native T cell receptors links residues of the polypeptide.

In the case of $\alpha\beta$ scTCRs or dTCRs displayed according to the invention, the requirement that the variable region sequences of the α and β segments are mutually orientated substantially as in native $\alpha\beta$ T cell receptors is tested by confirming that the molecule binds to the relevant TCR ligand (pMHC complex, CD1-antigen complex, superantigen or superantigen/pMHC complex) - if it binds, then the requirement is met. Interactions with pMHC complexes can be measured using a BIAcore 3000TM or

BIACore 2000™ instrument. WO99/6120 provides detailed descriptions of the methods required to analyse TCR binding to MHC-peptide complexes. These methods are equally applicable to the study of TCR/ CD1 and TCR/superantigen interactions. In order to apply these methods to the study of TCR/CD1 interactions 5 soluble forms of CD1 are required, the production of which are described in (Bauer (1997) Eur J Immunol 27 (6) 1366-1373). In the case of $\gamma\delta$ TCRs of the present invention the cognate ligands for these molecules are unknown therefore secondary means of verifying their conformation such as recognition by antibodies can be employed. The monoclonal antibody MCA991T (available from Serotec), specific for 10 the δ chain variable region, is an example of an antibody appropriate for this task.

The scTCRs or dTCRs of the present invention may be displayed on phage particles by, for example, the following two means:

15 (i) The C-terminus of one member of the dTCR polypeptide pair, or the C-terminus of the scTCR polypeptide, can be directly linked by a peptide bond to a surface exposed residue of the proteinaceous particle. For example, the said surface exposed residue is preferably at the N-terminus of the gene product of bacteriophage gene III or gene VIII; and

20 (ii) The C-terminus of one member of the dTCR polypeptide pair, or the C-terminus of the scTCR polypeptide, is linked by a disulfide bond to a surface exposed cysteine residue of the proteinaceous particle via an introduced cysteine residue. For example, the said surface exposed residue is again preferably at the N-terminus of the gene 25 product of bacteriophage gene III or gene VIII.

Method (i) above is preferred. In the case of a scTCR, nucleic acid encoding the TCR may be fused to nucleic acid encoding the particle forming protein or a surface protein of the replicable particle such as a phage. Alternatively, nucleic acid representing 30 mRNA-but-without-a-stop-codon,-or-fused-to-puromycin-RNA-may-be-translated-by ribosome such that the TCR remains fused to the ribosome particle. In the case of a

dTCR, nucleic acid encoding one chain of the TCR may be fused to nucleic acid encoding the particle forming protein or a surface protein of the replicable particle such as a phage, and the second chain of the TCR polypeptide pair may be allowed to associate with the resultant expressed particle displaying the first chain. Proper 5 functional association of the two chains is assisted by the presence of cysteines in the constant region of the two chains which are capable of forming an interchain disulfide bond, as more fully discussed below.

The displayed scTCR

10 The displayed scTCR polypeptide may be, for example, one which has a first segment constituted by an amino acid sequence corresponding to a TCR α or δ chain variable region sequence fused to the N terminus of an amino acid sequence corresponding to a TCR α chain constant region extracellular sequence,

15 a second segment constituted by an amino acid sequence corresponding to a TCR β or γ chain variable region fused to the N terminus of an amino acid sequence corresponding to TCR β chain constant region extracellular sequence,

20 a linker sequence linking the C terminus of the first segment to the N terminus of the second segment, or vice versa, and a disulfide bond between the first and second chains, said disulfide bond being one which has no equivalent in native $\alpha\beta$ or $\gamma\delta$ T cell receptors,

25 the length of the linker sequence and the position of the disulfide bond being such that the variable region sequences of the first and second segments are mutually orientated substantially as in native $\alpha\beta$ or $\gamma\delta$ T cell receptors.

The displayed dTCR

The dTCR which is displayed on the proteinaceous particle may be one which is constituted by

5 a first polypeptide wherein a sequence corresponding to a TCR α or δ chain variable region sequence is fused to the N terminus of a sequence corresponding to a TCR α chain constant region extracellular sequence, and

10 a second polypeptide wherein a sequence corresponding to a TCR β or γ chain variable region sequence fused to the N terminus a sequence corresponding to a TCR β chain constant region extracellular sequence,

the first and second polypeptides being linked by a disulfide bond which has no equivalent in native $\alpha\beta$ or $\gamma\delta$ T cell receptors.

15

dTCR Polypeptide Pair and scTCR Polypeptide

The constant region extracellular sequences present in the scTCRs or dTCRs preferably correspond to those of a human TCR, as do the variable region sequences. However, the correspondence between such sequences need not be 1:1 on an amino acid level. N- or C-truncation, and/or amino acid deletion and/or substitution relative to the corresponding human TCR sequences is acceptable, provided the overall result is mutual orientation of the α and β variable region sequences, or γ and δ variable region sequences is as in native $\alpha\beta$, or $\gamma\delta$ T cell receptors respectively. In particular, because the constant region extracellular sequences present in the first and second segments are not directly involved in contacts with the ligand to which the scTCR or dTCR binds, they may be shorter than, or may contain substitutions or deletions relative to, extracellular constant domain sequences of native TCRs.

The constant region extracellular sequence present in one of the dTCR polypeptide

30 pair, or in the first segment of a scTCR polypeptide may include a sequence

corresponding to the extracellular constant Ig domain of a TCR α chain, and/or the constant region extracellular sequence present in the other member of the pair or second segment may include a sequence corresponding to the extracellular constant Ig domain of a TCR β chain.

5

In one embodiment of the invention, one member of the polypeptide pair or the first segment of the scTCR polypeptide corresponds to substantially all the variable region of a TCR α chain fused to the N terminus of substantially all the extracellular domain of the constant region of an TCR α chain; and/or the other member of the pair or 10 second segment corresponds to substantially all the variable region of a TCR β chain fused to the N terminus of substantially all the extracellular domain of the constant region of a TCR β chain.

In another embodiment, the constant region extracellular sequences present in the 15 dTCR polypeptide pair or first and second segments of the scTCR polypeptide correspond to the constant regions of the α and β chains of a native TCR truncated at their C termini such that the cysteine residues which form the native inter-chain disulfide bond of the TCR are excluded. Alternatively those cysteine residues may be substituted by another amino acid residue such as serine or alanine, so that the native 20 disulfide bond is deleted. In addition, the native TCR β chain contains an unpaired cysteine residue and that residue may be deleted from, or replaced by a non-cysteine residue in, the β sequence of the scTCR of the invention.

In one particular embodiment of the invention, the TCR α and β chain variable region 25 sequences present in the dTCR polypeptide pair or first and second segments of the scTCR polypeptide may together correspond to the functional variable domain of a first TCR, and the TCR α and β chain constant region extracellular sequences present in the dTCR polypeptide pair or first and second segments of the scTCR polypeptide may correspond to those of a second TCR, the first and second TCRs being from the 30 same species. Thus the α and β chain variable region sequences present in dTCR

polypeptide pair or first and second segments of the scTCR polypeptide may correspond to those of a first human TCR, and the α and β chain constant region extracellular sequences may correspond to those of a second human TCR. For example, A6 Tax sTCR constant region extracellular sequences can be used as a framework onto which heterologous α and β variable domains can be fused.

In another embodiment of the invention, the TCR δ and γ chain variable region sequences present in the dTCR polypeptide pair or first and second segments of the scTCR polypeptide respectively, may together correspond to the functional variable domain of a first TCR, and the TCR α and β chain constant region extracellular sequences present in the dTCR polypeptide pair or first and second segments of the scTCR polypeptide respectively, may correspond to those of a second TCR, the first and second TCRs being from the same species. Thus the δ and γ chain variable region sequences present in the dTCR polypeptide pair or first and second segments of the scTCR polypeptide may correspond to those of a first human TCR, and the α and β chain constant region extracellular sequences may correspond to those of a second human TCR. For example, A6 Tax sTCR constant region extracellular sequences can be used as a framework onto which heterologous γ and δ variable domains can be fused.

In one particular embodiment of the invention, the TCR α and β , or δ and γ chain variable region sequences present in the dTCR polypeptide pair or first and second segments of the scTCR polypeptide may together correspond to the functional variable domain of a first human TCR, and the TCR α and β chain constant region extracellular sequences present in the dTCR polypeptide pair or first and second segments of the scTCR polypeptide may correspond to those of a second non-human TCR. Thus the α and β , or δ and γ chain variable region sequences present dTCR polypeptide pair or first and second segments of the scTCR polypeptide may correspond to those of a first human TCR, and the α and β chain constant region extracellular sequences may correspond to those of a second non-human TCR. For example, murine TCR constant

region extracellular sequences can be used as a framework onto which heterologous human α and β TCR variable domains can be fused.

Linker in the scTCR Polypeptide

5 For scTCR-displaying proteinaceous particles of the present invention, a linker sequence links the first and second TCR segments, to form a single polypeptide strand. The linker sequence may, for example, have the formula -P-AA-P- wherein P is proline and AA represents an amino acid sequence wherein the amino acids are glycine and serine.

10 For the scTCR displayed by proteinaceous particles of the present invention to bind to a ligand, MHC-peptide complex in the case of $\alpha\beta$ TCRs, the first and second segments must be paired so that the variable region sequences thereof are orientated for such binding. Hence the linker should have sufficient length to span the distance between the C terminus of the first segment and the N terminus of the second segment, or vice versa. On the other hand excessive linker length should preferably be avoided, in case the end of the linker at the N-terminal variable region sequence blocks or reduces bonding of the scTCR to the target ligand.

15

20 For example, in the case where the constant region extracellular sequences present in the first and second segments correspond to the constant regions of the α and β chains of a native TCR truncated at their C termini such that the cysteine residues which form the native interchain disulfide bond of the TCR are excluded, and the linker sequence links the C terminus of the first segment to the N terminus of the second segment, the linker may consist of from 26 to 41, for example 29, 30, 31 or 32 amino acids, and a particular linker has the formula -PGGG-(SGGGG)₅-P- wherein P is proline, G is glycine and S is serine.

25

Inter-chain Disulfide bond

30 A principle characterising feature of the scTCRs displayed by proteinaceous particles of the present invention, and preferably a feature of the displayed dTCRs, is the a

disulfide bond between the constant region extracellular sequences of the dTCR polypeptide pair or first and second segments of the scTCR polypeptide. That bond may correspond to the native inter-chain disulfide bond present in native dimeric $\alpha\beta$ TCRs, or may have no counterpart in native TCRs, being between cysteines 5 specifically incorporated into the constant region extracellular sequences of dTCR polypeptide pair or first and second segments of the scTCR polypeptide. In some cases, both a native and a non-native disulfide bond may be desirable.

10 The position of the disulfide bond is subject to the requirement that the variable region sequences of dTCR polypeptide pair or first and second segments of the scTCR polypeptide are mutually orientated substantially as in native $\alpha\beta$ or $\gamma\delta$ T cell receptors.

15 The disulfide bond may be formed by mutating non-cysteine residues on the first and second segments to cysteine, and causing the bond to be formed between the mutated residues. Residues whose respective β carbons are approximately 6 Å (0.6 nm) or less, and preferably in the range 3.5 Å (0.35 nm) to 5.9 Å (0.59 nm) apart in the native TCR are preferred, such that a disulfide bond can be formed between cysteine residues introduced in place of the native residues. It is preferred if the disulfide bond is between residues in the constant immunoglobulin region, although it could be between 20 residues of the membrane proximal region. Preferred sites where cysteines can be introduced to form the disulfide bond are the following residues in exon 1 of TRAC*01 for the TCR α chain and TRBC1*01 or TRBC2*01 for the TCR β chain:

TCR α chain	TCR β chain	Native β carbon separation (nm)
Thr 48	Ser 57	0.473
Thr 45	Ser 77	0.533
Tyr 10	Ser 17	0.359
Thr 45	Asp 59	0.560
Ser 15	Glu 15	0.59

Now that the residues in human TCRs which can be mutated into cysteine residues to form a new interchain disulfide bond in dTCRs or scTCRs displayed according to the invention have been identified, those of skill in the art will be able to mutate TCRs of other species in the same way to produce a dTCR or scTCR of that species for phage display. In humans, the skilled person merely needs to look for the following motifs in the respective TCR chains to identify the residue to be mutated (the shaded residue is the residue for mutation to a cysteine).

10	α Chain Thr 48:	DSDVYITDK T TVLDMRSMDFK (amino acids 39-58 of exon 1 of the TRAC*01 gene)
15	α Chain Thr 45:	QSKDSDVY T DKTVLDMRSM(amino acids 36-55 of exon 1 of the TRAC*01 gene)
20	α Chain Tyr 10:	DIQNPDP A V T QLRDSKSSDK(amino acids 1-20 of exon 1 of the TRAC*01 gene)
25	α Chain Ser 15:	DPAVYQLRD S KSSDKSVCLF(amino acids 6-25 of exon 1 of the TRAC*01 gene)
30	β Chain Ser 57:	NGKEVHSGV T D P QPLKEQP(amino acids 48- 67 of exon 1 of the TRBC1*01 & TRBC2*01 genes)
	β Chain Ser 77:	ALND S RYAL S SR L RVSATFW(amino acids 68- 87 of exon 1 of the TRBC1*01 & TRBC2*01 genes)
	β Chain Ser 17:	PPEVAVFEP S EA E ISHTQKA(amino acids 8- 27 of exon 1 of the TRBC1*01 & TRBC2*01 genes)
	β Chain Asp 59:	KEVHSGV T D P QPLKEQPAL(amino acids 50- 69 of exon 1 of the TRBC1*01 & TRBC2*01 genes gene)

β Chain Glu 15: VFPPEVAVFEPSEAEISHTQ (amino acids 6- 25 of exon 1 of the TRBC1*01 & TRBC2*01 genes)

5 In other species, the TCR chains may not have a region which has 100% identity to the above motifs. However, those of skill in the art will be able to use the above motifs to identify the equivalent part of the TCR α or β chain and hence the residue to be mutated to cysteine. Alignment techniques may be used in this respect. For example, ClustalW, available on the European Bioinformatics Institute website
 10 (<http://www.ebi.ac.uk/index.html>) can be used to compare the motifs above to a particular TCR chain sequence in order to locate the relevant part of the TCR sequence for mutation.

15 The present invention includes within its scope proteinaceous particle-displayed $\alpha\beta$ and $\gamma\delta$ -analogue scTCRs, as well as those of other mammals, including, but not limited to, mouse, rat, pig, goat and sheep. As mentioned above, those of skill in the art will be able to determine sites equivalent to the above-described human sites at which cysteine residues can be introduced to form an inter-chain disulfide bond. For example, the following shows the amino acid sequences of the mouse C α and C β
 20 soluble domains, together with motifs showing the murine residues equivalent to the human residues mentioned above that can be mutated to cysteines to form a TCR interchain disulfide bond (where the relevant residues are shaded):

Mouse C α soluble domain:

25 PYIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFTDKTVLDMK
 AMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVP

Mouse C β soluble domain:

EDLRNVTPPKVSLFEPSKAEIANKQKATLVCLARGFFPDHVELWWVNGREV
 30 HSGVSTDPOAYKESNYSYCLSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDK
 WPEGSPKPVTQNISAEAWGRAD

Murine equivalent of human α Chain Thr 48: ESGTFITDKT**E**VLDMKAMDSK

Murine equivalent of human α Chain Thr 45: KTMESGTF**I**DKT**E**VLDMKAM

5

Murine equivalent of human α Chain Tyr 10: YIQNPEPAV**I**QLKDPRSQDS

Murine equivalent of human α Chain Ser 15: AVYQLKDPR**S**QDSTLCLFTD

10

Murine equivalent of human β Chain Ser 57: NGREVHSGV**S**TDPQAYKESN

Murine equivalent of human β Chain Ser 77: KESNYSYCL**S**SRRLRVSATFW

Murine equivalent of human β Chain Ser 17: PPKVSLFEP**S**KAELANKQKA

15

Murine equivalent of human β Chain Asp 59: REVHSGV**S**TDPQAYKESNYS

Murine equivalent of human β Chain Glu 15: VTPPKVSLFEP**S**KAELANKQ

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As discussed above, the A6 Tax sTCR extracellular constant regions can be used as framework onto which heterologous variable domains can be fused. It is preferred that the heterologous variable region sequences are linked to the constant region sequences at any point between the disulfide bond and the N termini of the constant region sequences. In the case of the A6 Tax TCR α and β constant region sequences, the disulfide bond may be formed between cysteine residues introduced at amino acid residues 158 and 172 respectively. Therefore it is preferred if the heterologous α and β chain variable region sequence attachment points are between residues 159 or 173 and the N terminus of the α or β constant region sequences respectively.

25

TCR Display.

The preferred *in-vivo* TCR display method for biopanning to identify TCRs having desirable properties such as strong affinity for a target peptide-MHC complex is phage 5 display.

Firstly, a DNA library is constructed that encodes a diverse array of mutated scTCRs or dTCRs. This library is constructed by using DNA encoding a native TCR as the template for amplification. There are a number of suitable methods, known to those 10 skilled in the art, for the introduction of the desired mutations into the TCR DNA, and hence the finally expressed TCR protein. For example error-prone PCR (EP-TCR), DNA shuffling techniques, and the use of bacterial mutator strains such as XL-1-Red are convenient means of introducing mutations into the TCR sequences. It is particularly preferred if these mutations are introduced into defined regions of the 15 TCRs. For example, mutations in the variable region, particularly the complementarity-determining regions (CDRs) are likely to be the most appropriate sites for the introduction of mutations leading to the production of a diverse library of TCRs for the production of TCRs with enhanced ligand-binding properties. EP-PCR is an example of a method by which such 'region-specific' mutations can be introduced 20 into the TCRs. EP-PCR primers are used that are complementary to DNA sequences bordering the region to be mutated to amplify multiple copies of this region of the TCR DNA that contain a controllable level of random mutations. These DNA sequences encoding mutated regions are inserted into the DNA sequences, which encode the non-mutagenised sections of the TCR, by ligation or overlapping PCR.

25 The DNA encoding the TCR with mutated region can then be ligated onto DNA encoding a heterologous polypeptide in order to produce a fusion protein suitable for display. In the case of phage-display the expression vector utilised is either a phagemid or a phage gemone vector in which the TCR DNA can be ligated to DNA encoding the gIII or gVIII surface protein. In the case of a scTCR such ligation is 30 performed as for phage display of any monomeric peptide or polypeptide. In the case of dTCRs, only one of the TCR chains is ligated as aforesaid. The other chain is

encoded in nucleic acid for co-expression with the phagemid and helper phage nucleic acid, so that the expressed second chain finds and associates with the expressed phage with surface displayed first chain. In both cases, as discussed in more detail above, properly positioned cysteines in the constant regions are helpful in causing the variable 5 regions of the TCR to adopt their functional positions, through the formation of a disulfide bond by those cysteines.

For expression, the expression vectors comprising the TCR DNA library are then contacted with host cells capable of causing the expression of the encoded genetic 10 material under conditions suitable to allow the transformation of said cells. Such expression vectors and host cells harbouring them from additional aspects of the current invention.

The transformed cells are then incubated to allow the expression of the TCR- 15 displaying proteinaceous particles. These particles can then be used for screening or in assays to identify TCR variants with specific enhanced characteristics. Any particles that possess the enhanced characteristics under investigation can then be isolated. The DNA encoding these TCRs can then be amplified by PCR and the sequence determined.

20 It is known that high expression levels of an exogenous polypeptide may be toxic to the host cell. In such cases, either a host strain which is more tolerant of the exogenous polypeptide must be found, or the expression levels in the host cell must be limited to a level which is tolerated. For example (Beekwilder *et al.*, (1999) Gene 228 (1-2) 23- 25 31) report that only mutated forms of a potato protease inhibitor (PI2) which contained deletions or amber stop codons would be successfully selected from a phage display library. In the present case, an observation in the course of the work reported in the Examples herein suggests that it may be desirable to limit the expression levels of protein particle-displayed TCRs of the invention, at least in some strains of *E. coli*. 30 Thus, the A6 TCR selected in Example 4 after repeated rounds of culture was shown to be derived from cells in which the phagemid had mutated relative to that introduced

at the start. The mutation had created an 'opal' stop codon in the TCR β chain. This codon is 'read-through' with low frequency by ribosomes of the *E.coli* strain utilised resulting in the insertion of a tryptophan residue at this site and a much reduced overall level of full-length β chain expression.

5

There are several strategies for limiting the expression levels of an exogenous polypeptide from a given expression vector in a host which may be suitable for the limiting the expression levels of a scTCR, or one, or both TCR chains of a dTCR. For example:

10

Use of a weak promoter sequence – The level of expression obtained for a given gene product, such as the TCR α or β chain, can be tailored by using promoter sequences of varying strengths. The lambda phage P_{RM} promoter is an example of a weak promoter.

15

Mutated ribosome binding sites (RBS's) – Mutating a single nucleic acid in the RBS associated with a gene product, such as the TCR α or β chain, can result in a reduced level of expression. For example, mutating a wild-type AGGA sequence to AGGG.

20

Mutated 'start codons' - Mutating a single nucleic acid in the start codon associated with a gene product, such as the TCR α or β chain, can also result in a reduced level of expression. For example, mutating a wild-type AUG start codon to GUG.

25

Miss-sense suppressor mutations – These are inserted within the TCR β chain coding regions. Examples include the 'opal' stop codon (UGA), this 'leaky' stop codon results in the low frequency insertion of a tryptophan amino acid and read-through of the rest of the coding sequence.

Metabolite-mediated modification of promoter strength – The level of expression of a gene product, such as the TCR α or β chain, under the control of certain promoters can be down-regulated by the addition of a relevant metabolite to the cells containing the

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promoter. For example, glucose additions can be used to down-regulate expression of a gene product under the control of a Lac promoter.

Codon usage - Bacterial cells and, for example, mammalian cells have different 'preferences' relating to the codons they use to encode certain amino acids. For example, bacterial cells most commonly use the CGU codon to encode arginine whereas eucaryotic cells most commonly use AGA. It is possible to reduce the level of expression of a gene product, such as the TCR α or β chain, by utilising DNA sequences that contain a number of codons less preferred by the expression system being utilised.

Details relating to the above means of down-regulating gene product expression can be found in (Glass (1982) Gene Function – *E.coli* and its heritable elements, Croom Helm) and (Rezinoff (1980) The Operon 2nd Edition, Cold Spring Harbor Laboratory).

It is also known that supplying bacterial cultures with a relatively high concentration of a sugar such as sucrose can increase periplasmic expression levels of soluble proteins. (See for example (Sawyer *et al.*, (1994) Protein Engineering 7 (11) 1401-1406))

As mentioned above, for scTCR phage display, the scTCR polypeptide is expressed according to any of the three general prior art techniques discussed earlier as Methods A, B, and C. For the scTCRs displayed by phage particles of the present invention to bind to a ligand, MHC-peptide complex in the case of $\alpha\beta$ TCRs, the first and second segments must be paired so that the variable region sequences thereof are orientated for such binding. This correct pairing is assisted by the introduction of a disulfide bond in the extracellular constant region of the scTCR. Without wanting to be limited by theory, the novel disulfide bond is believed to provide extra stability to the scTCR during the folding process and thereby facilitating correct pairing of the first and second segments.

Also as mentioned above, for dTCR phage display, one of the dTCR polypeptide pair is expressed according to any of the three general prior art techniques discussed earlier as Methods A, B, and C as if it were eventually to be displayed as a monomeric polypeptide on the phage, and the other of the dTCR polypeptide pair is co-expressed in the same host cell. As the phage particle self assembles, the two polypeptides self associate for display as a dimer on the phage. Again, in the preferred embodiment of this aspect of the invention, correct folding during association of the polypeptide pair is assisted by a disulfide bond between the constant sequences, as discussed above. Further details of a procedure for phage display of a dTCR having an interchain disulfide bond appear in the Examples herein.

As an alternative, the phage displaying the first chain of the TCR may be expressed first, and the second chain polypeptide may be contacted with the expressed phage in a subsequent step, for association as a functional TCR on the phage surface.

The preferred *in-vitro* TCR display method for biopanning to identify TCRs having desirable properties such as strong affinity for a target peptide-MHC complex is ribosomal display of scTCRs.

Firstly, a DNA library is constructed that encodes a diverse array of mutated TCRs using the techniques discussed above. The DNA library is then contacted with RNA polymerase in order to produce a complementary mRNA library. Optionally, for mRNA display techniques the mRNA sequences can then be ligated to a DNA sequence comprising a puromycin binding site. These genetic constructs are then contacted with ribosomes *in-vitro* under conditions allowing the translation of the scTCR polypeptide. These scTCR-displaying ribosomes can then be used for screening or in assays to identify TCR variants with specific enhanced characteristics. Any particles that possess the enhanced characteristics under investigation can then be isolated. The mRNA encoding these TCRs can then be converted to the complementary DNA sequences using reverse transcriptase. This DNA can then be amplified by PCR and the sequence determined.

Additional Aspects

5 A proteinaceous particle displaying a scTCR or dTCR (which preferably is constituted by constant and variable sequences corresponding to human sequences) of the present invention may be provided in substantially pure form, or as a purified or isolated preparation. For example, it may be provided in a form which is substantially free of other proteins.

10 10 A phage particle displaying a plurality of scTCRs or dTCRs of the present invention may be provided in a multivalent complex. Thus, the present invention provides, in one aspect, a multivalent T cell receptor (TCR) complex, which comprises a phage particle displaying a plurality of scTCRs or dTCRs as described herein. Each of the plurality of said scTCRs or dTCRs is preferably identical.

15 15 In a further aspect, the invention provides a method for detecting TCR ligand complexes, which comprises:

- a. providing a TCR-displaying proteinaceous particle of the current invention
- b. contacting the TCR-displaying phage with the putative ligand complexes; and

20 20 detecting binding of the TCR-displaying proteinaceous particle to the putative ligand complexes.

25 25 TCR ligands suitable for identification by the above method include, but are not limited to, peptide-MHC complexes.

Isolation of TCR variants with enhanced characteristics

30 30 A further aspect of the invention is a method for the isolation of TCRs with a specific enhanced characteristic, said method comprising subjecting a diverse library of TCRs displayed on proteinaceous particles to an assay which measures said characteristic and thereby identifying those proteinaceous particles which display a TCR with the

desired enhancement and isolating these proteinaceous particles. The DNA sequences encoding the variant TCRs can then be obtained and amplified by PCR to allow the sequences to be determined. The characteristics that can be enhanced include, but are not limited to, ligand binding affinity and construct stability.

5

Screening Use

The TCR-displaying proteinaceous particles of the present invention are capable of utilisation in screening methods designed to identify modulators, including inhibitors, of the TCR-mediated cellular immune synapse.

10

As is known to those skilled in the art there are a number of assay formats that provide a suitable basis for protein-protein interaction screens of this type.

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Amplified Luminescent Proximity Homogeneous Assay systems such as the AlphaScreen™, rely on the use of "Donor" and "Acceptor" beads that are coated with a layer of hydrogel to which receptor and ligand proteins can be attached. The interaction between these receptor and ligand molecules brings the beads into proximity. When these beads are subject to laser light a photosensitizer in the "Donor" bead converts ambient oxygen to a more excited singlet state. The singlet state oxygen molecules diffuse across to react with a chemiluminescer in the "Acceptor" bead that further activates fluorophores contained within the same bead. The fluorophores subsequently emit light at 520-620 nm, this signals that the receptor-ligand interaction has occurred. The presence of an inhibitor of the receptor-ligand interaction causes this signal to be diminished.

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Surface Plasmon Resonance (SPR) is an interfacial optical assay, in which one binding partner (normally the receptor) is immobilised on a 'chip' (the sensor surface) and the binding of the other binding partner (normally the ligand), which is soluble and is caused to flow over the chip, is detected. The binding of the ligand results in an increase in concentration of protein near to the chip surface which causes a change in the refractive index in that region. The surface of the chip is comprised such that the

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change in refractive index may be detected by surface plasmon resonance, an optical phenomenon whereby light at a certain angle of incidence on a thin metal film produces a reflected beam of reduced intensity due to the resonant excitation of waves of oscillating surface charge density (surface plasmons). The resonance is very sensitive to changes in the refractive index on the far side of the metal film, and it is this signal which is used to detect binding between the immobilised and soluble proteins. Systems which allow convenient use of SPR detection of molecular interactions, and data analysis, are commercially available. Examples are the IasysTM machines (Fisons) and the BiacoreTM machines.

10

Other interfacial optical assays include total internal reflectance fluorescence (TIRF), resonant mirror (RM) and optical grating coupler sensor (GCS), and are discussed in more detail in Woodbury and Venton (*J. Chromatog. B.* **725** 113-137 (1999)).

15

The scintillation proximity assay (SPA) has been used to screen compound libraries for inhibitors of the low affinity interaction between CD28 and B7 (K_d probably in the region of 4 μM (Van der Merwe *et al* *J. Exp. Med.* **185**:393-403 (1997), Jenh *et al*, *Anal Biochem* **165**(2) 287-93 (1998)). SPA is a radioactive assay making use of beta particle emission from certain radioactive isotopes which transfers energy to a scintillant immobilised on the indicator surface. The short range of the beta particles in solution ensures that scintillation only occurs when the beta particles are emitted in close proximity to the scintillant. When applied for the detection of protein-protein interactions, one interaction partner is labelled with the radioisotope, while the other is either bound to beads containing scintillant or coated on a surface together with scintillant. If the assay can be set up optimally, the radioisotope will be brought close enough to the scintillant for photon emission to be activated only when binding between the two proteins occurs.

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A further aspect of the invention is a method of identifying an inhibitor of the interaction between a TCR-displaying proteinaceous particle of the invention, and a TCR-binding ligand comprising contacting the TCR-displaying proteinaceous particle with a TCR-binding ligand, in the presence of and in the absence of a test compound,

and determining whether the presence of the test compound reduces binding of the TCR-displaying proteinaceous particle to the TCR-binding ligand, such reduction being taken as identifying an inhibitor.

5 A further aspect of the invention is a method of identifying a potential inhibitor of the interaction between an TCR-displaying proteinaceous particle of the invention, and a TCR-binding ligand, for example a MHC-peptide complex, comprising contacting the TCR-displaying proteinaceous particle or TCR-binding ligand partner with a test compound and determining whether the test compound binds to the TCR-displaying proteinaceous particle and/or the TCR-binding ligand, such binding being taken as identifying a potential inhibitor. This aspect of the invention may find particular utility

10 in interfacial optical assays such as those carried out using the BIACore™ system.

High Affinity TCRs

15 The present invention also makes available mutated TCRs specific for a given TCR ligand with higher affinity for said TCR ligand than the wild-type TCR. These high affinity TCRs are expected to be particularly useful for the diagnosis and treatment of disease.

20 Where used herein the term 'high affinity TCR' is defined as any mutated sc or dTCR of the present invention which interacts with a specific TCR ligand and either: has a Kd for the said TCR ligand less than that of the native TCR as measured by Surface Plasmon Resonance.

25 Or

has an off-rate (k_{off}) for the said TCR ligand less than that of the native TCR as measured by Surface Plasmon Resonance.

High affinity scTCRs or dTCRs of the present invention are preferably mutated relative to the native TCR in at least one complementarity determining region.

In one aspect of the present invention the TCR ligand for which a given high affinity
5 TCR is specific is a pMHC.

In a further aspect of the present invention the TCR ligand for which a given high affinity TCR is specific is the HLA-A2 tax peptide (LLFGYPVYV) complex.

10 One or both of the high affinity TCR chains may be labelled with a detectable label, for example a label that is suitable for diagnostic purposes. Thus, the invention provides a method for detecting a TCR ligand selected from CD1-antigen complexes, bacterial superantigens, and MHC-peptide/superantigen complexes which method comprises contacting the TCR ligand with a high affinity TCR or multimeric high affinity TCR complex in accordance with the invention which is specific for the TCR ligand; and detecting binding of the high affinity TCR or multimeric high affinity TCR complex to the TCR ligand. In tetrameric high affinity TCR complexes formed using biotinylated heterodimers, fluorescent streptavidin (commercially available) can be used to provide a detectable label. A fluorescently-labelled tetramer is suitable for use
15 in FACS analysis, for example to detect antigen presenting cells carrying the peptide for which the high affinity TCR is specific.

20

Another manner in which the soluble high affinity TCRs of the present invention may be detected is by the use of TCR-specific antibodies, in particular monoclonal
25 antibodies. There are many commercially available anti-TCR antibodies, such as α Fl and β Fl, which recognise the constant regions of the α and β chain, respectively.

The high affinity TCR (or multivalent complex thereof) of the present invention may alternatively or additionally be associated with (e.g. covalently or otherwise linked to)
30 a therapeutic agent which may be, for example, a toxic moiety for use in cell killing, or an immunostimulating agent such as an interleukin or a cytokine. A multivalent

high affinity TCR complex of the present invention may have enhanced binding capability for a TCR ligand compared to a non-multimeric wild-type or high affinity T cell receptor heterodimer. Thus, the multivalent high affinity TCR complexes according to the invention are particularly useful for tracking or targeting cells

5 presenting particular antigens *in vitro* or *in vivo*, and are also useful as intermediates for the production of further multivalent high affinity TCR complexes having such uses. The high affinity TCR or multivalent high affinity TCR complex may therefore be provided in a pharmaceutically acceptable formulation for use *in vivo*.

10 The invention also provides a method for delivering a therapeutic agent to a target cell, which method comprises contacting potential target cells with a high affinity TCR or multivalent high affinity TCR complex in accordance with the invention under conditions to allow attachment of the high affinity TCR or multivalent high affinity TCR complex to the target cell, said high affinity TCR or multivalent high affinity TCR complex being specific for the TCR ligand and having the therapeutic agent associated therewith.

15

20 In particular, the soluble high affinity TCR or multivalent high affinity TCR complex can be used to deliver therapeutic agents to the location of cells presenting a particular antigen. This would be useful in many situations and, in particular, against tumours. A therapeutic agent could be delivered such that it would exercise its effect locally but not only on the cell it binds to. Thus, one particular strategy envisages anti-tumour molecules linked to high affinity T cell receptors or multivalent high affinity TCR complexes specific for tumour antigens.

25

30 Many therapeutic agents could be employed for this use, for instance radioactive compounds, enzymes (perforin for example) or chemotherapeutic agents (cis-platin for example). To ensure that toxic effects are exercised in the desired location the toxin could be inside a liposome linked to streptavidin so that the compound is released slowly. This will prevent damaging effects during the transport in the body and ensure

that the toxin has maximum effect after binding of the TCR to the relevant antigen presenting cells.

Other suitable therapeutic agents include:

- 5 • small molecule cytotoxic agents, i.e. compounds with the ability to kill mammalian cells having a molecular weight of less than 700 daltons. Such compounds could also contain toxic metals capable of having a cytotoxic effect. Furthermore, it is to be understood that these small molecule cytotoxic agents also include pro-drugs, i.e. compounds that decay or are converted under physiological conditions to release cytotoxic agents. Examples of such agents include cis-platin, maytansine derivatives, rachelmycin, calicheamicin, docetaxel, etoposide, gemcitabine, ifosfamide, irinotecan, melphalan, mitoxantrone, sorfimer sodiumphotofrin II, temozolamide, topotecan, trimetreate glucuronate, auristatin E vincristine and doxorubicin;
- 10 • peptide cytotoxins, i.e. proteins or fragments thereof with the ability to kill mammalian cells. Examples include ricin, diphtheria toxin, pseudomonas bacterial exotoxin A, DNAase and RNAase;
- 15 • radio-nuclides, i.e. unstable isotopes of elements which decay with the concurrent emission of one or more of α or β particles, or γ rays. Examples include iodine 131, rhenium 186, indium 111, yttrium 90, bismuth 210 and 213, actinium 225 and astatine 213; chelating agents may be used to facilitate the association of these radio-nuclides to the high affinity TCRs, or multimers thereof;
- 20 • prodrugs, such as antibody directed enzyme pro-drugs;
- 25 • immuno-stimulants, i.e. moieties which stimulate immune response. Examples include cytokines such as IL-2, chemokines such as IL-8, platelet factor 4, melanoma growth stimulatory protein, etc, antibodies or fragments thereof, complement activators, xenogeneic protein domains, allogeneic protein domains, viral/bacterial protein domains and viral/bacterial peptides.

30 Soluble high affinity TCRs or multivalent high affinity TCR complexes of the invention may be linked to an enzyme capable of converting a prodrug to a drug. This

allows the prodrug to be converted to the drug only at the site where it is required (i.e. targeted by the sTCR).

5 A multitude of disease treatments can potentially be enhanced by localising the drug through the specificity of soluble high affinity TCRs. For example, it is expected that the high affinity HLA-A2-tax (LLFGYPVYV) specific A6 TCR disclosed herein may be used in methods for the diagnosis and treatment of HTLV-1.

10 Viral diseases for which drugs exist, e.g. HIV, SIV, EBV, CMV, would benefit from the drug being released or activated in the near vicinity of infected cells. For cancer, the localisation in the vicinity of tumours or metastasis would enhance the effect of toxins or immunostimulants. In autoimmune diseases, immunosuppressive drugs could be released slowly, having more local effect over a longer time-span while minimally affecting the overall immuno-capacity of the subject. In the prevention of 15 graft rejection, the effect of immunosuppressive drugs could be optimised in the same way. For vaccine delivery, the vaccine antigen could be localised in the vicinity of antigen presenting cells, thus enhancing the efficacy of the antigen. The method can also be applied for imaging purposes.

20 The soluble high affinity TCRs of the present invention may be used to modulate T cell activation by binding to specific TCR ligand and thereby inhibiting T cell activation. Autoimmune diseases involving T cell-mediated inflammation and/or tissue damage would be amenable to this approach, for example type I diabetes. Knowledge of the specific peptide epitope presented by the relevant pMHC is required for this use.

25 Medicaments in accordance with the invention will usually be supplied as part of a sterile, pharmaceutical composition which will normally include a pharmaceutically acceptable carrier. This pharmaceutical composition may be in any suitable form, (depending upon the desired method of administering it to a patient). It may be provided 30 in unit dosage form, will generally be provided in a sealed container and may be provided

as part of a kit. Such a kit would normally (although not necessarily) include instructions for use. It may include a plurality of said unit dosage forms.

5 The pharmaceutical composition may be adapted for administration by any appropriate route, for example by the oral (including buccal or sublingual), rectal, nasal, topical (including buccal, sublingual or transdermal), vaginal or parenteral (including subcutaneous, intramuscular, intravenous or intradermal) route. Such compositions may be prepared by any method known in the art of pharmacy, for example by admixing the active ingredient with the carrier(s) or excipient(s) under sterile conditions.

10 Pharmaceutical compositions adapted for oral administration may be presented as discrete units such as capsules or tablets; as powders or granules; as solutions, syrups or suspensions (in aqueous or non-aqueous liquids; or as edible foams or whips; or as emulsions). Suitable excipients for tablets or hard gelatine capsules include lactose, maize starch or derivatives thereof, stearic acid or salts thereof. Suitable excipients for 15 use with soft gelatine capsules include for example vegetable oils, waxes, fats, semi-solid, or liquid polyols etc.

20 For the preparation of solutions and syrups, excipients which may be used include for example water, polyols and sugars. For the preparation of suspensions oils (e.g. vegetable oils) may be used to provide oil-in-water or water in oil suspensions.

25 Pharmaceutical compositions adapted for transdermal administration may be presented as discrete patches intended to remain in intimate contact with the epidermis of the recipient for a prolonged period of time. For example, the active ingredient may be delivered from the patch by iontophoresis as generally described in *Pharmaceutical Research*, 3(6):318 (1986). Pharmaceutical compositions adapted for topical administration may be formulated as ointments, creams, suspensions, lotions, powders, solutions, pastes, gels, sprays, aerosols or oils. For infections of the eye or other external tissues, for example mouth and skin, the compositions are preferably applied as a topical ointment or cream. 30 When formulated in an ointment, the active ingredient may be employed with either a paraffinic or a water-miscible ointment base. Alternatively, the active ingredient may be

formulated in a cream with an oil-in-water cream base or a water-in-oil base.

Pharmaceutical compositions adapted for topical administration to the eye include eye drops wherein the active ingredient is dissolved or suspended in a suitable carrier, especially an aqueous solvent. Pharmaceutical compositions adapted for topical administration in the mouth include lozenges, pastilles and mouth washes.

5 Pharmaceutical compositions adapted for rectal administration may be presented as suppositories or enemas. Pharmaceutical compositions adapted for nasal administration wherein the carrier is a solid include a coarse powder having a particle size for example

10 in the range 20 to 500 microns which is administered in the manner in which snuff is taken, i.e. by rapid inhalation through the nasal passage from a container of the powder held close up to the nose. Suitable compositions wherein the carrier is a liquid, for administration as a nasal spray or as nasal drops, include aqueous or oil solutions of the active ingredient. Pharmaceutical compositions adapted for administration by inhalation

15 include fine particle dusts or mists which may be generated by means of various types of metered dose pressurised aerosols, nebulizers or insufflators. Pharmaceutical compositions adapted for vaginal administration may be presented as pessaries, tampons, creams, gels, pastes, foams or spray formulations. Pharmaceutical compositions adapted for parenteral administration include aqueous and non-aqueous sterile injection solution

20 which may contain anti-oxidants, buffers, bacteriostats and solutes which render the formulation substantially isotonic with the blood of the intended recipient; and aqueous and non-aqueous sterile suspensions which may include suspending agents and

thickening agents. Excipients which may be used for injectable solutions include water, alcohols, polyols, glycerine and vegetable oils, for example. The compositions may be

25 presented in unit-dose or multi-dose containers, for example sealed ampoules and vials, and may be stored in a freeze-dried (lyophilized) condition requiring only the addition of the sterile liquid carried, for example water for injections, immediately prior to use.

Extemporaneous injection solutions and suspensions may be prepared from sterile powders, granules and tablets.

The pharmaceutical compositions may contain preserving agents, solubilising agents, stabilising agents, wetting agents, emulsifiers, sweeteners, colourants, odourants, salts (substances of the present invention may themselves be provided in the form of a pharmaceutically acceptable salt), buffers, coating agents or antioxidants. They may also 5 contain therapeutically active agents in addition to the substance of the present invention.

Dosages of the substances of the present invention can vary between wide limits, depending upon the disease or disorder to be treated, the age and condition of the individual to be treated, etc. and a physician will ultimately determine appropriate 10 dosages to be used. The dosage may be repeated as often as appropriate. If side effects develop the amount and/or frequency of the dosage can be reduced, in accordance with normal clinical practice.

The invention also provides a method for obtaining a high affinity TCR chain, which 15 method comprises incubating such a host cell under conditions causing expression of the high affinity TCR chain and then purifying the polypeptide.

Preferred features of each aspect of the invention are as for each of the other aspects 20 *mutatis mutandis*. The prior art documents mentioned herein are incorporated to the fullest extent permitted by law.

Examples

The invention is further described in the following examples, which do not limit the scope of the invention in any way.

25 Reference is made in the following to the accompanying drawings in which:

Figures 1a and 1b show respectively the nucleic acid sequences of a soluble A6 TCR α and β chains, mutated so as to introduce a cysteine codon. The shading indicates the 30 introduced cysteine codons.

Figure 2a shows the A6 TCR α chain extracellular amino acid sequence, including the $T_{48} \rightarrow C$ mutation (underlined) used to produce the novel disulphide inter-chain bond, and Figure 2b shows the A6 TCR β chain extracellular amino acid sequence, including the $S_{57} \rightarrow C$ mutation (underlined) used to produce the novel disulphide inter-chain bond.

5

Figure 3 Outlines the cloning of TCR α and β chains into phagemid vectors. The diagram describes a phage display vector. RSB is the ribosome-binding site. S1 or S2 are signal peptides for secretion of proteins into periplasm of *E. coli*. The * indicates 10 translation stop codon. Either of the TCR α chain or β chain can be fused to phage coat protein, however in this diagram only TCR β chain is fused to phage coat protein.

Figure 4 details the DNA sequence of phagemid pEX746:A6.

15

Figure 5 expression of phage particle fusions of bacterial coat protein and heterodimeric A6 TCR in *E. coli*. Fusion proteins of heterodimeric A6 TCR::gIII are detected using western blotting. Phage particles are prepared from *E. coli* XL-1-Blue and concentrated with PEG/NaCl. The samples are loaded in reducing or non-reducing sample buffers. Lane 1 is the sample of clone 7 containing correct sequence, and lane 20 2 is the sample of clone 14 containing a deletion in the α -chain encoding gene. The heterodimeric A6 TCR:gIII fusion protein was detected at 125kDa.

25

Figure 6 illustrates ELISA detection of pMHC peptide complex binding activity of a heterodimeric A6 TCR displayed on phage. Clone 7 binds specifically to HLA A2-Tax complex. Clone 14 cannot bind to any pMHC, as no TCR is attached to the phage particles.

Figure 7a schematic illustration of the single-chain A6 TCR-C-Kappa DNA ribosome display construct.

Figure 7b details the complete DNA and amino acid sequences of the single-chain A6 TCR-C-Kappa DNA ribosome display construct encoded in pUC19.

Figure 8 details the DNA sequence of pUC19-T7.

5

Figure 9 details the DNA sequence of the single-chain A6 TCR-C-Kappa ribosome display construct that was cloned into pUC19-T7.

10

Figure 10 Western blot showing the detection of in-vitro translated single-chain A6 TCR-C-Kappa using Ambion rabbit reticulocyte lysates.

Figure 11 RT-PCR of the single-chain A6 TCR-C-Kappa mRNA on beads rescued from the ribosome display reactions.

15

Figure 12a details the DNA sequence of the A6 TCR Clone 9 mutated β chain; the mutated nucleic acid is indicated in bold.

Figure 12b details the amino acid sequence of the A6 TCR Clone 9 mutated β chain, the position corresponding to the introduced opal stop codon is indicated with an *.

20

Figure 13 details the DNA sequence of the A6 TCR Clone 49 mutated β chain; the mutated nucleic acid is indicated in bold. As this is a 'silent' mutation no change is introduced into the resulting amino acid sequence by this mutation.

25

Figure 14a details the DNA sequence of the A6 TCR Clone 134 mutated A6 TCR β chain; the mutated nucleic acids are indicated in bold.

30

Figure 14b details the amino acid sequence of the A6 TCR Clone 134 mutated A6 TCR β chain as tested by BIACore assay; the mutated amino acids are indicated in bold.

Figure 14c details the amino acid sequence of the A6 TCR Clone 134 mutated A6 TCR β chain as tested by phage ELISA assay; the mutated amino acids are indicated in bold.

5 Figure 15 BIACore data for the binding of A6 TCR clone 134 to HLA-A2 Tax and HLA-A2 NY-ESO

Figure 16 BIACore data used to determine T_{OFF} for the binding of A6 TCR clone 134 to HLA-A2 Tax

10 Figures 17a and 17b show the DNA sequence of the mutated α and β chains of the NY-ESO TCR respectively

15 Figures 18a and 18b show the amino acid sequences of the mutated α and β chains of the NY-ESO TCR respectively

Figure 19 details the DNA and amino acid sequence of the NY-ESO TCR β chain as incorporated into the pEX746:NY-ESO phagemid respectively.

20 Figure 20 shows the specific binding of phage particles displaying the NY-ESO TCR to HLA-A2-NY-ESO in a phage ELISA assay.

25 Figure 21 shows the DNA sequence of the DR1 α chain incorporating codons encoding the Fos dimerisation peptide attached to the 3' end of the DRA0101 sequence. Shading indicates the Fos codons and the biotinylation tag codons are indicated by in bold text.

30 Figure 22 shows the DNA sequence of the pAcAB3 bi-cistronic vector used for the expression of Class II HLA-peptide complexes in Sf9 insect cells. The Bgl II restriction site (AGATCT) used to insert the HLA α chain and the BamHI restriction site (GGATCC) used to insert the HLA β chain are indicated by shading.

Figure 23 shows the DNA sequence of the DR1 β chain incorporating codons encoding the Jun dimerisation peptide attached to the 3' end of the DRB0401

sequence and codons encoding an HLA-loaded peptide attached to the 5' end of the DRB0401 sequence. Shading indicates the Jun codons, and the HLA-loaded Flu HA peptide codons are underlined.

5 Figure 24 shows a BIACore trace of the binding of the high affinity A6 TCR clone 134 to flowcells coated as follows:

Flow-cell 1 (FC 1) - Blank

Flow-cell 2 (FC 2) - HLA-A2 (LLGRNSFEV)

Flow-cell 3 (FC 3) - HLA-A2 (KLVALGINAV)

10 Flow-cell 4 (FC 4) - HLA-A2 (LLGDLFGV)

Figure 25 shows a BIACore trace of the binding of the high affinity A6 TCR clone 134 to flowcells coated as follows:

Flow-cell 1 (FC 1) - Blank

15 Flow-cell 2 (FC 2) - HLA-B8 (FLRGRAYGL)

Flow-cell 3 (FC 3) - HLA-B27 (HRCQAIRKK)

Flow-cell 4 (FC 4) - HLA- Cw6 (YRSGIIAVV)

Figure 26 shows a BIACore trace of the binding of the high affinity A6 TCR clone 134 to flowcells coated as follows:

Flow-cell 1 (FC 1) - Blank

Flow-cell 2 (FC 2) - HLA-A24 (VYGFVRACL)

Flow-cell 3 (FC 3) - HLA-A2 (ILAKFLHWL)

Flow-cell 4 (FC 4) - HLA-A2 (LTLGEFLKL)

25 Figure 27 shows a BIACore trace of the binding of the high affinity A6 TCR clone 134 to flowcells coated as follows:

Flow-cell 1 (FC 1) - Blank

Flow-cell 2 (FC 2) - HLA-DR1 (PKYVKQNTLKLA)

30 Flow-cell 3 (FC 3) - HLA-A2 (GILGFVFTL)

Flow-cell 4 (FC 4) - HLA-A2 (SLYNTVATL)

Figure 28 shows a BIACore trace of the binding of the high affinity A6 TCR clone 134 to flowcells coated as follows:

Flow-cell 1 (FC 1) – Blank

Flow-cell 4 (FC 4) - HLA-A2 (LLFGYPVYV)

5

Example 1 – Design of primers and mutagenesis of A6 Tax TCR α and β chains to introduce the cysteine residues required for the formation of a novel inter-chain disulphide bond

10 For mutating A6 Tax threonine 48 of exon 1 in TRAC*01 to cysteine, the following primers were designed (mutation shown in lower case):

5'-C ACA GAC AAA tgT GTG CTA GAC AT
5'-AT GTC TAG CAC Aca TTT GTC TGT G

15

For mutating A6 Tax serine 57 of exon 1 in both TRBC1*01 and TRBC2*01 to cysteine, the following primers were designed (mutation shown in lower case):

20 5'-C AGT GGG GTC tGC ACA GAC CC
5'-GG GTC TGT Gca GAC CCC ACT G

PCR mutagenesis:

Expression plasmids containing the genes for the A6 Tax TCR α or β chain were mutated using the α -chain primers or the β -chain primers respectively, as follows.

25

100 ng of plasmid was mixed with 5 μ l 10 mM dNTP, 25 μ l 10xPfu-buffer (Stratagene), 10 units Pfu polymerase (Stratagene) and the final volume was adjusted to 240 μ l with H₂O. 48 μ l of this mix was supplemented with primers diluted to give a final concentration of 0.2 μ M in 50 μ l final reaction volume. After an initial denaturation step of 30 seconds at 95°C, the reaction mixture was subjected to 15 rounds of denaturation (95°C, 30 sec.), annealing (55°C, 60 sec.), and elongation (73°C, 8 min.) in a Hybaid PCR express PCR machine. The product was then digested

30

for 5 hours at 37°C with 10 units of DpnI restriction enzyme (New England Biolabs). 10 μ l of the digested reaction was transformed into competent XL1-Blue bacteria and grown for 18 hours at 37°C. A single colony was picked and grown over night in 5 ml TYP + ampicillin (16 g/l Bacto-Tryptone, 16 g/l Yeast Extract, 5 g/l NaCl, 2.5 g/l K₂HPO₄, 100 mg/l Ampicillin). Plasmid DNA was purified on a Qiagen mini-prep column according to the manufacturer's instructions and the sequence was verified by automated sequencing at the sequencing facility of Department of Biochemistry, Oxford University. The respective mutated nucleic acid and amino acid sequences are shown in Figures 1a and 2a for the α chain and Figures 1b and 2b for the β chain.

10

Example 2 – Construction of phage display vectors and cloning of A6 TCR α and β chains into the phagemid vectors.

In order to display a heterodimeric A6 TCR containing a non-native disulfide inter-chain bond on filamentous phage particles, phagemid vectors were constructed for expression of fusion proteins comprising the heterodimeric A6 TCR containing a non-native disulfide inter-chain bond with a phage coat protein. These vectors contain a pUC19 origin, an M13 origin, a bla (Ampicillin resistant) gene, Lac promoter/operator and a CAP-binding site. The design of these vectors is outlined in Figure 3, which 15 describes vectors encoding for both the A6 TCR β chain-gp3 or A6 TCR β chain-gp8 fusion proteins in addition to the soluble A6 TCR α chain. The expression vectors containing the DNA sequences of the mutated A6 TCR α and β chains incorporating the additional cysteine residues required for the formation of a novel disulfide inter-chain bond prepared in Example 1 and as shown in figures 1a and 1b were used as the 20 source of the A6 TCR α and β chains for the production of a phagemid encoding this TCR. The complete DNA sequence of the phagemid construct (pEX746) utilised is 25 given in Figure 4.

The molecular cloning methods for constructing the vectors are described in 30 "Molecular cloning: A laboratory manual, by J. Sambrook and D. W. Russell".

Primers listed in table-1 are used for construction of the vectors. A example of the PCR programme is 1 cycle of 94°C for 2 minutes, followed by 25 cycles of 94°C for 5 seconds, 53°C for 5 seconds and 72°C for 90 seconds, followed by 1 cycles of 72°C for 10 minutes, and then hold at 4°C. The Expand hifidelity Taq DNA polymerase is purchased from Roche.

Table 1. Primers used for construction of the A6 TCR phage display vectors

Primer name	Sequence 5' to 3'
YOL1	TAATAATACGTATAATAATATTCTATTCAAG GAGACAGTC
YOL2	CAATCCAGCGGCTGCCGTAGGCAATAGGTATT TCATTATGACTGTCTCCTTGAAATAG
YOL3	CtaCGGCAGCCGCTGGATTGTTATTACTCGCG GCCCGCCGGCCATGGCccag
YOL4	GTTCTGCTCCACTTCCTCTGGGCCATGGCG GCTGGGCCG
YOL5	CAGAAGGAAGTGGAGCAGAAC
YOL6	CTTCTTAAAGAATTCTTAATTAAACCTAGGTTA TTAGGAACCTTCTGGGCTGGGAAG
YOL7	GTAAATTAAAGAATTCTTAAGAAGGAGATATA CATATGAAAAATTATTATTCGCAATT
YOL8	CGCGCTGTGAGAATAGAAAGGAACAACAAAG GAATTCGCGAATAATAATTTTTTTTCAATATG
YOL9	CTTTCTATTCTCACAGCGCGCAGGCTGGTGT ACTCAGAC
YOL10	ATGATGTCTAGATGCGGCCGCGTCTGCTCTAC CCCAGGGCTC
YOL11	GCATCTAGACATCATCACCATCATCACTAGAC TGTTGAAAGTTGTTAGCAAAAC
YOL12	CTAGAGGGTACCTTATTAAGACTCCTTATTAC GCAGTATG

Example 3 – Expression of fusions of bacterial coat protein and heterodimeric A6 TCR in E. coli.

In order to validate the construct made in Example 2, phage particles displaying the heterodimeric A6 TCR containing a non-native disulfide inter-chain bond were prepared using methods described previously for the generation of phage particles displaying antibody scFvs (Li *et al*, 2000, Journal of Immunological Methods 236: 133-146) with the following modifications. *E. coli* XL-1-Blue cells containing pEX746:A6 phagemid (i.e. the phagemid encoding the soluble A6 TCR α chain and an A6 TCR β chain fused to the phage gIII protein produced as described in Example 2) were used to inoculate 5 ml of Lbatg (Lennox L broth containing 100 μ g/ml of ampicillin, 12.5 μ g/ml tetracycline and 2% glucose), and then the culture was incubated with shaking at 37°C overnight (16 hours). 50 μ l of the overnight culture was used to inoculate 5 ml of TYPatg (TYP is 16g/l of peptone, 16g/l of yeast extract, 5g/l of NaCl and 2.5g/l of K₂HPO₄), and then the culture was incubated with shaking at 37°C until OD_{600nm} = 0.8. Helper phage M13 K07 was added to the culture to the final concentration of 5 X 10⁹ pfu/ml. The culture was then incubated at 37°C stationary for thirty minutes and then with shaking at 200 rpm for further 30 minutes. The medium of above culture was then changed to TYPak (TYP containing 100 μ g/ml of ampicillin, 25 μ g/ml of kanamycin), the culture was then incubated at 25°C with shaking at 250 rpm for 36 to 48 hours. The culture was then centrifuged at 4°C for 30 minutes at 4000 rpm. The supernatant was filtrated through a 0.45 μ m syringe filter and stored at 4°C for further concentration or analysis.

The fusion protein of filamentous coat protein and heterodimeric A6 TCR containing a non-native disulfide inter-chain bond was detected in the supernatant by western blotting. Approximately 10¹¹ cfu phage particles were loaded on each lane of an SDS-PAGE gel in both reducing and non-reducing loading buffer. Separated proteins were primary-antibody probed with an anti-M13 gIII mAb, followed by a second antibody conjugated with Horseradish Peroxidase (HRP). The HRP activity was then detected with Opti-4CN substrate kit from Bio-Rad (Figure 5). These data indicated that

disulfide-bonded A6 TCR of clone 1 is fused with filamentous phage coat protein, gIII protein.

5 *Example 4 – Detection of functional heterodimeric A6 TCR containing a non-native disulfide inter-chain bond on filamentous phage particles*

The presence of functional (HLA-A2-tax binding) A6 TCR displayed on the phage particles was detected using a phage ELISA method.

10 *TCR-Phage ELISA*

Binding of the A6 TCR-displaying phage particles to immobilised peptide-MHC in ELISA is detected with primary rabbit anti-fd antisera (Sigma) followed by alkaline phosphatase (AP) conjugated anti-Rabbit mAb (Sigma). Non specific protein binding sites in the plates can be blocked with 2% MPBS or 3% BSA-PBS

15 *Materials and reagents*

1. Coating buffer, PBS
2. PBS: 138mM NaCl, 2.7mM KCl, 10mM Na₂HPO₄, 2mM KH₂PO₄
3. MPBS , 3% marvel-PBS
4. PBS-Tween: PBS, 0.1% Tween-20
5. Substrate solution, Sigma FAST pNPP, Cat# N2770

Method

1. Rinse NeutrAvidin coated wells twice with PBS.
- 25 2. Add 25µl of biotin-HLA-A2 Tax or biotin-HLA-A2 NYESO in PBS at concentration of 10 µg/ml, and incubate at room temperature for 30 to 60 min.
3. Rinse the wells twice with PBS
4. Add 300 µl of 3% Marvel-PBS, and incubate at room temperature for 1hr. Mix the TCR-phage suspension with 1 volume of 3% Marvel-PBS and incubate at

30 room temperature.

5. Rinse the wells twice with PBS
6. Add 25 μ l of the mixture of phage-A6 TCR/Marvel-PBS, incubate on ice for 1hr
7. Rinse the wells three times with ice-cold PBStween, and three times with ice-cold PBS.
8. Add 25 μ l of ice cold rabbit anti-fd antibody diluted 1:1000 in Marvel-PBS, and incubate on ice for 1hr
9. Rinse the wells three times with ice-cold PBStween, and three times with ice-cold PBS.

10 10. Add 25 μ l of ice cold anti-rabbit mAb-Ap conjugate diluted 1:50,000 in Marvel-PBS, and incubate on ice for 1hr

11. Rinse the wells three times with ice-cold PBStween, and three times with ice-cold PBS.

12. Add 150 μ l of Alkaline phosphatase yellow to each well and read the signal at 405nm

The results presented in Figure 6 indicate clone 1 produced a phage particle displaying an A6 TCR that can bind specifically to its cognate pMHC. (HLA-A2 Tax)

Analysis of the DNA sequence of this displayed A6 TCR revealed the presence of an 'opal' stop codon in the TCR β chain not present in the corresponding sequence of the expression vector construct of Example 2. This codon is 'read-through' with low frequency by ribosomes of the *E.coli* strain utilised resulting in the insertion of a tryptophan residue at this site and a much-reduced overall level of full-length β chain expression. From this observation it was inferred that only cells expressing this mutated A6 TCR sequence had survived the culture rounds of Example 3, and that

therefore the high levels of A6 TCR predicted to be expressed by the original expression vector were toxic to the host cells.

Example 5 – single- chain TCR (scTCR) ribosome display

5

Construction of Ribosome display scTCR vectors for use in generation of ribosome display PCR templates.

Ribosome display constructs were cloned into the readily available DNA plasmid pUC19 in order to generate an error free and stable DNA PCR template from which to 10 conduct subsequent ribosome display experiments. Vector construction was undertaken in two steps so as to avoid the use of large oligonucleotide primers (with their associated error problems). The final A6 scTCR-C-Kappa DNA ribosome display construct is shown in a schematic form in figure 7a and both DNA and protein sequences are shown in Figure 7b. This construct can be excised from pUC19 as a 15 Pst1/EcoR1 double digest.

The molecular cloning methods for constructing the vectors are described in “Molecular cloning: A laboratory manual, by J. Sambrook and D. W. Russell”. Primers listed in Table 2 are used for construction of the vectors. The PCR programme 20 utilised was as follows – 1 cycle of 94°C for 2 minutes, followed by 25 cycles of 94°C for 30 seconds, 55°C for 20 seconds and 72°C for 120 seconds, followed by 1 cycles of 72°C for 5 minutes, and then hold at 4°C. The Pfu DNA polymerase is purchased from Strategene. Oligonucleotide primers used are described in table 2.

25 *Construction of pUC19-T7- Step 1*

The construction of pUC19-T7 is described below; the construction results in a pUC19 vector containing a T7 promoter region followed by a short space region and the an optimum eukaryotic Kozak sequence. This is an essential part of the ribosome display 30 construct as it is required for the initiation of transcription of any attached sequence in rabbit reticulocyte lysates. Sequences for ribosome display such as the A6scTCR-

C_{kappa} can be ligated into the pUC19-T7 vector between the NcoI and EcoR1 restriction sites.

Equimolar amounts of the primer Rev-link and For-link were annealed by heating to 5 94°C for 10 min and slowly cooling the reaction to room temperature. This results in the formation of a double stranded DNA complex that can be seen below.

5' AGCTGCAGCTAATACGACTCACTATAGAACAGGCCACCATGG
CGTCGATTATGCTGAGTGATATCCTGTCCGGTGGTACCCCTAG 3'

10

The 5' region contains an overhanging sticky end complimentary to a HindIII restriction site whilst the 3' end contains a sticky end that is complimentary to a BamH1 restriction site.

15 The annealed oligonucleotides were ligated into Hind III/BamH1 double-digested pUC19 which had been purified by agarose gel electrophoresis, excised and further purified with the Qiagen gel extraction kit. The ligations were transformed into *E. coli* XL1-BLUE. Individual pUC19-T7 clones were sequenced to confirm the presence of the correct sequence. The sequence is shown in Figure 8.

20

Construction of A6scTCR-C-Kappa vector – Step 2.

Construction of the single chain A6scTCR-C-Kappa DNA sequence requires the generation of three PCR fragments that must then be assembled into one A6scTCR-C-25 Kappa fragment. The fragments consist of (a.) the A6 TCR alpha chain variable region flanked by a NcoI site in the 5' region and a section of Glycine Serine linker in the 3' region flanked by a BamH1 restriction site. This product was generated via a standard PCR of the vector pEX202 with the primers 45 and 50 (See Table 2). Fragment (b.) A6 TCR beta variable and constant region flanked by a BamH1 restriction site in the 30 5' region followed by a section of Glycine Serine linker. This product was generated via a standard PCR of the vector pEX207 with the primers 72 and 73 (See Table 2).

Fragment (c.) Portion of a human C-kappa region generated by a standard PCR of the p147 vector with the primers 61-60 (See Table 2). All PCR products were run on a 1.6% TBE agarose gel and DNA bands of the correct size excised and purified using the Qiagen gel extraction kit.

5 Fragments (b.) and (c.) were fused by a standard overlap PCR via the complementarity in their primer sequences 73 and 61(See Table 2). The PCR was carried out via the primers 72 and 60 (See Table 2). The PCR products were run on a 1.6% TBE agarose gel and DNA bands of the correct size excised and purified using the Qiagen gel extraction kit. This fragment is termed (d.).

10 Fragment (a.) was double digested with Nco1 and BamH1 whilst fragment (d.) was double digested with BamH1 and EcoR1. pUC19-T7 was double digested with Nco1 and EcoR1. All digested DNA products were run on a 1.2% TBE agarose gel and DNA bands of the correct size were excised and purified using the Qiagen gel extraction kit. The digested pUC19-T7, fragments (a.) and (d.) were ligated and 15 transformed into E. coli XL1-BLUE. Transformants were sequenced to confirm the correct sequence. The sequence of the A6scTCR-C-Kappa ribosome display construct that was cloned into pUC19 is shown in Figure 9 flanked by its Pst1 and EcoR1 sites.

20

25

30

Table 2.

Oligonucleotides used (Purchased from MWG).

Rev-Link	5' GATCCCATGGTGGCCTGTTCCCTATAGTGAGTCGTATTAGCTGC
For-Link	5' AGCTGCAGCTAATACGACTCACTATAGGAACAGGCCACCATGG
45-A6	5' CCACCATGGGCCAGAAGGAAGTGGAGCAGAACTC
7 A6-Beta(RT-PCR)(a)	5' CGAGAGCCCGTAGAACTGGACTTG
49-A6-BamH1-F	5' GTGGATCCGGCGGTGGCGGGTCGAACGCTGGTGTCA CTCAGACCCC
50-A6-BamH1-R	5' CCGGATCCACCTCCGCCTGAACCGCCTCCACCGGTGACCACAAAC CTGGGTCCCTG
60-Kappa-rev-EcoR1	5' CTGAGAATTCTTATGACTCTCCGCGGTTGAAGCTC
61-Betac-Kappa-for1	5' TGACGAATTCTGACTCTCCGCGGTTGAAGCTC
71 T7-Primer	5' AGCTGCAGCTAATACGACTCACTATAGG
72 A6-beta	5' GGCCACCATGGCAACGCTGGTGTCACTCAGACCCC
73-A6-cons-rev	5' TGAACCGCCTCCACCGTCTGCTCTACCCAGGCCTCGGCG
75 Kappa-rev	5' TGACTCTCCGCGGTTGAAGCTC

5 *Demonstration of the production of sc A6 TCR-C-Kappa by In vitro transcription translation.*

Preparation of scA6 TCR-C-Kappa PCR product for In vitro transcription translation.

10 Here we describe the synthesis of sc A6 TCR-C-Kappa via *In vitro* transcription translation in the presence of biotinylated lysine and its subsequent detection by western blotting and detection with alkaline phosphatase labelled streptavidin.

15 The sc A6 TCR-C-Kappa PCR product was prepared in a standard PCR reaction using the vector sc A6 TCR-C-Kappa as template and PCR primers 71 and 60. Primer 60 contains a stop codon to allow the release of the scTCR from the ribosome. Pfu

polymerase (Strategene) was used for increased fidelity during PCR synthesis. The PCR products were run on a 1.6% TBE agarose gel and DNA bands of the correct size excised and purified using the Qiagen gel extraction kit.

The transcription translation reactions were carried out using the Ambion

5 PROTEINscript II Linked transcription translation kit Cat 1280-1287 with 300ng of the above described PCR product. Three transcription translation reactions were set up according to the manufactures protocol. The one modification was the addition of biotinylated lysine from the Transcend™ Non-Radioactive Translation Detection System.

10

Reaction 1 sc A6 TCR-C-Kappa 300ng with 2µl biotinylated lysine

Reaction 2 sc A6 TCR-C-Kappa 300ng without 2µl biotinylated lysine

Reaction 3 No DNA control with 2µl biotinylated lysine.

15

Two microliters of each reaction was run on a 4-20% Novex gradient SDS-PAGE gel (Invitrogen). Additionally a number of dilutions of a control biotinylated TCR were also run. The gel was blotted and the proteins detected with streptavidin alkaline phosphatase and subsequently colometrically developed with Western Blue ® Stabilized Substrate for Alkaline Phosphatase as described in the Transcend™ Non-

20

Radioactive Translation Detection System protocol. The western blot is shown in Figure 10.

In the no DNA control and A6scTCR-C-Kappa reaction without biotinylated lysine no band of approximately the correct size can be seen as expected whilst in the A6scTCR-C-Kappa reaction in the presence of biotinylated lysine a band of

25

approximately the correct size can be seen. This demonstrates the synthesis of the sc A6 TCR-C-Kappa TCR by *In vitro* transcription translation.

Preparation of sc A6 TCR-C-Kappa ribosome display PCR product.

30

The sc-A6-TCR-C-Kappa-PCR-product-was-prepared-in-a-standard-PCR-reaction-using the vector A6scTCR-C-Kappa as template and PCR primers 71 and 75 (See Table 2).

Primer 75 does not contain a stop codon. Pfu polymerase (Strategene) was used for increased fidelity during PCR synthesis. The PCR products were run on a 1.6% TBE agarose gel and DNA bands of the correct size were excised and purified using the Qiagen gel extraction kit.

5

Ribosome Display Process

Transcription and translation of sc A6 TCR-C-Kappa

10 The transcription / translation reactions were carried out using the Ambion PROTEINscript II Linked transcription translation kit (Cat No. 1280-1287)

Transcription reactions

The following transcription reactions were set up in Ambion 0.5 ml non stick tubes (Cat No. 12350).

15

Contents	tube 1 (Normal A6)	2 (Control)
Water	4.53 µl	5.7µl
Template (PCR product)	Sc A6 TCR-C-Kappa PCR product 1.17µl (300 ng)	No DNA
5X transcription mix	2 µl	2µl
Enzyme mix	2µl	2µl
Superasin _{ambion} RNase inhibitor	0.3µl	0.3µl
Final volume	10µl	10µl

The tubes were incubated at 30°C for 60 min on a PCR block with the hot lid off.

5 *Translation reactions*

The following translation reactions were set up in Ambion 0.5 ml non stick tubes.

Contents	1 (Normal A6)	2 (Control)
Reticulocyte Lysate	105µl	105 µl
25mM Mg-Acetate	3µl	3 µl
Translation Mix	7.5µl	7.5 µl
Methionine	7.5µl	7.5 µl
Water	18µl	18 µl
Superasin <small>Rnase inhibitor</small>	3µl	3 µl
Transcription reaction	6µl tube 1 above	6µl tube 2 above

10 Each tube contains enough for 3x50µl selections. The tubes were mixed and incubated at 30°C for 60 min on a PCR block with the hot lid off. After 30 min 3 Unit of RQ1 Rnase free Dnase (Promega) was added to destroy the original DNA template in tube 1 and 3 Unit RQ1 Rnase free Dnase (Promega) in tube 2. After 60 min 18µl of Heparin solution was added to translation reaction 2 and 18µl of Heparin solution was added to translation reaction 1. Samples were stored on ice ready for selection against HLA-coated beads.

15

Coating of magnetic beads.

20µl of resuspended Streptavidin Magnetic Particles (Roche Cat. No. 1641778) were transferred into a sterile Rnase free 1.5 ml eppendorf tube. The beads were immobilised with a Magnetic Particle Separator (Roche Cat. No. 1641794) and the supernatant was removed. The beads were then washed with 100 µl of Rnase free 1 X

PBS (10 x PBS Ambion Cat No. 9624, Ambion H₂O Cat No. 9930) the beads were immobilised and the supernatant was removed. A total of 3 PBS washes were carried out.

5 The beads were resuspended in 20 μ l of PBS and the contents split evenly between two tubes (10 μ l each). One tube will be used to produce control-blocked beads and the other tubes to produce HLA-A2-Tax coated beads.

10 To the control beads tube 80 μ l of BSA/Biotin solution was added and mixed. The BSA/Biotin solution was made up as follows. 10 μ l of a 0.2M Tris base 0.1M Biotin solution was added to 990 μ l of PBS 0.1 % BSA (Ambion Ultrapure Cat No. 2616). Also 20 μ l of Heparin solution (138 mg/ml Heparin (Sigma H-3393) in 1 x PBS) was added and the solution mixed. The beads were incubated at room temperature for 1 hour with intermittent mixing. The beads were then washed three times with 100 μ l of PBS and were resuspended in 10 μ l of PBS, 0.1% BSA.

15 The HLA-TAX coated beads were prepared as follows. 40 μ l of HLA-A2-Tax(1.15 mg/ml prepared as described in WO99/60120) was added to the 10 μ l of beads and mixed. The beads were incubated at room temperature for 15 min and then 20 μ l of BSA 50mg/ml Ambion Cat 2616 and 20 μ l of heparin solution (see above) were added 20 and mixed. The beads were incubated for a further 45 min and then 20 μ l of BSA/Biotin solution was added. The beads were then washed three times with 100 μ l of PBS and were re-suspended in 10 μ l of PBS, 0.1% BSA.

Panning with magnetic beads

25 The sc A6 TCR translation reaction was split into three 50 μ l aliquots and each aliquot received either 2 μ l of the following beads:

Control (no HLA)

HLA-A2-Tax

30 HLA-A2-Tax plus 10 μ g soluble scA6 TCR

A control translation reaction was also carried out and split into three 50 μ l aliquots and each aliquot received either 2 μ l of the following beads

5 Control (no HLA)
HLA-A2-Tax
HLA-A2-Tax plus 10 μ g soluble sc A6 TCR

This gave a total of six tubes. The tubes were incubated on a PCR block at 5°C for 60
10 min with intermittent mixing.

The beads were then washed three times with 100 μ l ice cold buffer (PBS, 5mM Mg-acetate, 0.2% Tween 20(Sigma Rnase free). Each aliquot of beads were then re-suspended in 50 μ l of 1 x RQ1 Dnase digestion buffer containing 1 μ l (40 U) of
15 Superasin and 1 μ l (1U) of RQ1 Dnase. The beads were incubated on a PCR block for 30 min at 30°C.

The beads were then washed three times with 100 μ l ice cold buffer (PBS, 5mM Mg-acetate, 0.2% Tween 20) and once with ice cold H₂O. The beads were re-suspended in
20 10 μ l of Rnase free H₂O. The beads were then frozen ready for RT-PCR.

RT-PCR of sc A6 TCR-C-Kappa mRNA on beads rescued from the ribosome display reactions.

25 The RT PCR reactions on the beads were carried out using the Titan one tube RT-PCR kit cat 1855476 as described in the manufacturers protocols. Two microliters of beads were added into each RT-PCR reaction along with the primers 45 and 7 and 0.3 μ l of Superasin Rnase inhibitor.
For each RT-PCR reaction a second PCR only reaction was set up which differed only
30 by the fact that no reverse transcriptase was present just Roche high fidelity polymerase. This second reaction served as a control for DNA contamination.

Additionally a RT-PCR positive control control was set up using 1ng of the vector sc A6 TCR-C-Kappa.

5 The reactions were cycled as follows. An RT-PCR step was carried out by incubation of the samples at 50°C for 30 min followed by the inactivation of the reverse transcriptase by incubation at 94°C for 3 min on a PCR block.

The reactions were PCR cycles as follows for a total of 38 cycles:

94°C 30 seconds

10 55°C 20 seconds

68°C 130 seconds.

The PCR reaction was finished by incubation at 72°C for 4 minutes.

Great care was taken during all ribosome display steps to avoid Rnase contamination.

15 The RT-PCR and PCR reactions were run on a 1.6% TBE agarose gel which can be seen in Figure 11. Analysis of the gel shows that there is no DNA contamination and that all PCR products are derived from mRNA. The DNA band of the correct size in lane 2 demonstrates that ribosome displayed sc A6 TCR-C-Kappa was selected out by HLA-A2-Tax coated beads. Lane 3 shows that we can inhibit this specific selection of 20 ribosome-displayed sc A6 TCR-C-Kappa by the addition of soluble sc A6 TCR. The significant reduction in the band intensity in lane 3 relative to the uninhibited sample in lane 2 demonstrates this. No binding of ribosome-displayed sc A6 TCR-C-Kappa could be shown against control non-HLA coated beads.

25 *Example 6 – Sequence Analysis of A6 TCR clones displayed on phage particles and methods to improve display characteristics*

After the construction of vectors for displaying A6 TCR on phage by PCR and molecular cloning, bacterial clones that can produce phage particles displaying A6 TCR were screened by phage ELISA as described in Example 4. Three different 30 clones were identified that gave specific binding to HLA-A2-tax in the ELISA binding

assay. These clones all contained mutations in the 'wild-type' A6 TCR DNA or in the associated regulatory sequences, which are described in the following table:

Functional clones from screening TCR A6 displayed on phage

Name	Feature	
Clone 7	The third ribosome-binding site, which is located in front of $\nu\beta$ gene, is mutated from <u>AAGGAGA</u> to <u>AAGGGGA</u> .	
Clone 9	An opal codon is introduced in $\nu\beta$ CDR3.	Full DNA and amino acid sequence in Figures 12a & 12b
Clone 49	An amber codon is introduced in $\nu\beta$ FR1. This mutation introduces a 'silent' mutation that does not affect the resulting amino acid sequence	Full DNA sequence in Figures 13a

5

These clones all contained mutations that are likely to cause a reduction in the expression levels of the A6 TCR β chain. It was inferred that low expression clones were selected over high expression clones as a result of cell toxicity caused by high expression levels of TCR.

10

Example 7—Mutagenesis of A6 TCR CDR3 regions

The CDR3 regions of the A6 TCR were targeted for the introduction of mutations to investigate the possibility of generating high affinity mutants.

15

Overlapping PCR was used to modify the sequence of α and β CDR3 regions to introduce two unique restriction sites *Hind III* for α chain, with oligos of YOL54,

5'CAGCTGGGGAAAGCTTCAGTTGGAGCAG3', and YOL55,

5'CTGCTCCAAACTGAAGCTTCCCCCAGCTG3', and *Xho I* for β chain, with

oligos of YOL56 5'GTACTTCTGTGCCTCGAGGCCGGACTAG3' and YOL57 5'CTAGTCCCGGCCTCGAGGCACAGAAGTAC3'.

PCR was used to introduce mutations for affinity maturation. The A6 TCR clone 9 (incorporating an introduced opal codon in the β chain CDR3 sequence) was used as a source of template DNA, and TCR chains were amplified with the mutation primers (detailed in the following table) and YOL22 5'CATTTCAGGGATAGCAAGC3' (β -chains) or YOL13 5'TCACACAGGAAACAGCTATG3' (α -chains).

10 Primers for introducing mutation at CDR3 of A6 β chain and α chain

Primer name	Sequence 5' to 3'
YOL59	TGTGCCTCGAGGNNKNNKNNKNNKNNK NKCGACCAGAGCAGTACTTCG
YOL60	TGTGCCTCGAGGCCGNNKNNKNNKNNK NKNNKCCAGAGCAGTACTTCGGC
YOL61	TGTGCCTCGAGGCCGNNKNNKNNKNNK NKNNKCGACCAGAGCAGTACTTCG
YOL62	TGTGCCTCGAGGCCGNNKNNKNNKNNK NKNNKGGAGGGCGACCAGAGCAG
YOL63	TGTGCCTCGAGGCCGGGANNKNNKNNK NKNNKNNKGGCGACCAGAGCAGTAC
YOL68	TGTGCCTCGAGGNNKNNKNNKNNKNNK NKCCAGAGCAGTACTTCGggc
YOL69	TGTGCCTCGAGGNNKNNKNNKNNKNNK NKGAGCAGTACTTCGggccg
YOL70	TGTGCCTCGAGGNNKNNKNNKNNKNNK NKCAGTACTTCGggccggc
YOL71	TGTGCCTCGAGGccgNNKNNKNNKNNK ggCGACCAGAGCAGTACTTCG
YOL58	AAACTGAAGCTTMNNMNNMNNMNNMNT GTAACGGCACAGAGGTAG
YOL72	AAACTGAAGCTTMNNMNNNgctgtcMNNT GTAACGGCACAGAGGTAG
YOL73	AAACTGAAGCTTMNNMNNMNNNgctgtcM NNTGTAACGGCACAGAGGTAG
YOL74	AAACTGAAGCTTMNNMNNNgctgtcMNNA ACGGCACAGAGGTAG

α -chain fragments were digested with *Nco I* and *HindIII* and re-purified using a Qiagen kit and vector was prepared by digesting clone 9 with *Nco I* and *HindIII* followed by gel purification using a Qiagen kit. β -chain fragments were digested with

Xho I and *Not I* and re-purified using a Qiagen kit and vector was prepared by digesting clone 9 with *Xho I* and *Not I* followed by gel purification using a Qiagen kit. Purified inserts and vectors at 3:1 molar ratio were mixed with T4 ligase buffer, T4 ligase and nuclease-free water. The ligations were carried out at 16°C water bath overnight. For each mutation-library, a total of 0.5 to 1µg purified ligated products were electroporated into *E. coli* TG1 at ratio of 0.2µg DNA per 40 µl of electroporation-competent cells (Stratagen) following the protocols provided by the manufacturer. After electroporation, the cells were re-suspended immediately with 960µl of SOC medium at 37°C and plated on a 244mm x244mm tissue culture plate containing YTE (15g Bacto-Agar, 8g NaCl, 10g Tryptone, 5g Yeast Extract in 1 litre) supplemented with 100µg/ml ampicillin and 2% glucose. The plate was incubated at 30°C over night. The cells were then scraped from the plates with 5 ml of DYT (16g Tryptone, 10g Yeast extract and 5g NaCl in 1 litre, autoclaved at 125°C for 15 minutes) supplemented with 15% glycerol.

15 In order to make phage particles displaying the A6 TCR, 500 ml of DYTak (DYT containing 100 µg/ml of ampicillin and 2% glucose) was inoculated with 500 to 1000 µl of the library stocks. The culture was grown until OD(600nm) reached 0.5. 100 ml of the culture was infected with helper phage (M13 K07 (Invitrogen), or HYPER 20 PHAGE (Progen Biotechnik, GmbH 69123 Heidelberg), and incubated at 37°C water bath for 30 minutes. The medium was replaced with 100 ml of DYTak (DYT containing 100 µg/ml ampicillin and 25 µg/ml of kanamycin). The culture was then incubated with shaking at 300 rpm and 25°C for 20 to 36 hours.

25 *Example 8 – Isolation of high affinity A6 TCR mutants*

The isolation of high affinity A6 TCR mutants was carried out using two different methods.

30 The first method involves selecting phage particles displaying mutant A6 TCRs capable of binding to HLA-A2 Tax complex using Maxisorp immuno-tubes

(Invitrogen) The immuno-tubes were coated with 1 to 2 ml 10 μ g/ml streptavidin in PBS overnight at room temperature. The tubes were washed twice with PBS, and then 1 ml of biotinylated HLA-A2 Tax complex at 5 μ g/ml in PBS was added and incubated at room temperature for 30 minutes. The rest of the protocol for selection of high affinity binders is as described previously (Li *et al.* (2000) *Journal of Immunological Methods* 236: 133-146), except for the following modifications. The selection was performed over three or four rounds. The concentrations of biotinylated HLA-A2 Tax complex were 5 μ g/ml for the first round of selection, 0.5 μ g/ml for the second, 0.05 μ g/ml for the third and 0.005 μ g/ml for the fourth round of selection. M13 K07 helper phage were used in rounds one and two, and hyper phage were used in subsequent rounds, for the selection.

The second method utilised was the selection of phage particles displaying mutant A6 TCRs capable of binding to HLA-A2 Tax complex in solution. Streptavidin-coated paramagnetic beads (Dynal M280) were pre-washed according to manufacturer's protocols. Phage particles, displaying mutated A6 TCR at a concentration of 10¹² to 10¹³ cfu, were pre-mixed with biotinylated HLA-A2 Tax complex at concentrations of 2x10⁻⁸M, 2x10⁻⁹M, 2x10⁻¹⁰M and 2x 10⁻¹¹M for first, second, third and fourth-round of selections respectively. The mixture of A6 TCR-displaying phage particles and HLA-A2 Tax complex was incubated for one hour at room temperature with gentle rotation, and A6 TCR-displaying phage particles bound to biotinylated HLA-A2 Tax complex were captured using 200 μ l (round 1) or 50 μ l (round 2, 3, and 4) of streptavidin-coated M280 magnetic beads. After capture of the phage particles, the beads were washed a total of ten times (three times in PBS _{Tween20}, twice in PBS _{Tween 20} containing 2% skimmed milk powder, twice in PBS, once in PBS containing 2% skimmed milk powder, and twice in PBS) using a Dynal magnetic particle concentrator. After final wash, the beads was re-suspended in 1ml of freshly prepared 100mM triethylamine pH11.5, and incubated for 5 to 10 minutes at room temperature with gentle rotation. Phage particles eluted from the beads were neutralized immediately with 300 μ l of 1M tris-HCl pH7.0. Half of the eluate was used to infect 10 ml of *E.coli* TG1 at OD(600nm)=0.5 freshly prepared for the amplification of the selected phage particles

according to the methods previously described (Li *et al.*, (2000) *Journal of Immunological Methods* 236: 133-146).

After the third or fourth round of selection, 95 colonies were picked from the plates
5 and used to inoculate 100 μ l of DYTag in a 96-well microtiter plate. The culture was
incubated at 37°C with shaking overnight. 100 μ l of DYTag was then sub-inoculated
with 2 to 5 μ l of the overnight cultures, and incubated at 37°C with shaking for 2 to 3
hours or until the culture became cloudy. To infect the cells with helper phage, the
culture was infected with 25 μ l of DYTag containing 5×10^9 pfu helper phages, and
10 incubated at 37°C for 30 minutes. The medium was replaced with DYTak. The plates
were incubated at 25°C for 20 to 36 hours with shaking at 300 rpm. The cells were
precipitated by centrifugation at 3000g for 10 minutes at 4°C. Supernatants were used
to screen for high affinity A6 TCR mutants by competitive phage ELISA as follows.

15 Nunc-Immuno Maxisorp wells coated with streptavidin were rinsed twice with PBS.
25 μ l 5 μ g/ml biotinylated HLA-A2-Tax complex was added to each well and these
were incubated at room temperature for 30 to 60 minutes, and followed by two PBS
rinses. Non-specific protein binding sites in the wells were blocked by the addition of
300 μ l 3% skimmed milk in PBS followed by incubation at room temperature for 2
20 hours. In order to prepare phage particles displaying the heterodimeric A6 TCR, phage
particles were mixed with 3% skimmed milk in PBS containing 0, 20, and 200 nM
HLA-A2-Tax, followed by incubated at room temperature for 1 hour. The phage is
added to the wells coated with HLA-A2-Tax and incubated at room temperature for 1
hour, followed by 3 washes with PBS containing 0.1% tween 20 and then 3 washes
25 with PBS. The bound TCR-dispaying phage particles are detected with an anti-fd
antibody (Sigma) as described in Example 4.

Several high affinity A6 TCR mutants were identified, and the CDR3 sequences are
listed in the two following tables along with the corresponding wild-type sequences.
Amber-stop-codons (*) were found in all β -chain mutants and one α -chain mutant.

A6 TCR β chain mutants

clone	CDR3 sequence
Wild Type	GCCTCGAGGCCGGACTAGCGGGAGGGCGACCAGAGCAGTAG A S R P G L A G G R P E Q Y
134	GCCTCGAGGCCGGGCTGATGAGTGCCTAGCCAGAGCAGTAC A S R P G L M S A * P E Q Y
86	GCCTCGAGGCCGGGCTGAGGTCGGCTAGCCAGAGCAGTAC A S R P G L R S A * P E Q Y
87	GCCTCGAGGCCGGACTAGCGGGAGGGCGACCAGAGCGTAG A S R P G L A G G R P E A *
89	GCCTCGAGGCCGGACTAGCGGGAGGGCGACCAGAGGATTAG A S R P G L A G G R P E D *
85	GCCTCGAGGCCGGACTAGCGGGAGGGCGACCAGATCAGTAG A S R P G L A G G R P D Q *
83	GCCTCGAGGCCGGGCTGTAGGCTGGCGACCAGAGCAGTAC A S R P G L * A G R P E Q Y
1	GCCTCGAGGCCGGGCTGGTCCGGGCGACCAGAGCAGTAG A S R P G L V P G R P E Q *
2	GCCTCGAGGCCGGGCTGTGTCTGCTTAGCCAGAGCAGTAC A S R P G L V S A * P E Q Y
111	GCCTCGAGGCCGGACTAGCGGGAGGGCGACCACATCCGTAG A S R P G L A G G R P H P *
125	GCCTCGAGGCCGGACTAGCGGGAGGGCGACCAGATCGTAG A S R P G L A G G R P D A *
133	GCCTCGAGGCCGGGCTGATTAGTGCTTAGCCAGAGCAGTAC A S R P G L I S A * P E Q Y

A6 TCR α chain mutants

Clone	CDR3
Wild Type	GCCGTTACAAC TGACAGCTGGGGGAAGCTTCAG A V T T D S W G K L Q
149	GCCGTTACAAC TGACAGCTGGGGCGCTTCAG A V T T D S W G P L Q
65	GCCGTTACAAC TGACAGCTGGGGGAAGATGCAG A V T T D S W G K M Q
66	GCCGTTACAAC TGACAGCTGGGGGAAGTTGCAT A V T T D S W G K L H
153	GCCGTTACAAC TGACAGCTGGGGTAGCTTCAT A V T T D S W G * L H
71	GCCGTTACAAC TGACAGCTGGGGGAGCTTCAT A V T T D S W G E L H
70	GCCGTTACAAC TGACAGCTGGGGAGGCTGCAT A V T T D S W G R L H
121	GCCGTTACAAC TGACAGCTGGGGCAGCTTCAT A V T T D S W G Q L H

117	GCCGTTACAAC TGACAGCTGGGGGAAGGTTCAT A V T T D S W G K V H
72	GCCGTTACAAC TGACAGCTGGGGGAAGGTGAAT A V T T D S W G K V N
150	GCCGTTACAAC TGACAGCTGGGGGAAGCTTCTG A V T T D S W G K L L

Example 9 – Production of soluble heterodimeric A6 TCR with non-native disulfide bond between constant regions, containing CDR3 mutations

Phagemid DNA encoding the high affinity A6 TCR mutants identified in Example 8 was isolated from the relevant *E.coli* cells using a Mini-Prep kit (Qiagen, UK)

10 PCR amplification using the phagemid DNA as a target and the following primers was used to amplify the soluble TCR α and β chain DNA sequences.

A6 TCR alpha chain forward primer
ggaattc atcgatg cagaaggaagtggagcag
15 Clal restriction site is underlined)

Universal TCR alpha chain reverse primer
gtacacggccgggtcagggttctggatatac
(EagI restriction site is underlined)

20

A6 beta chain forward primer
tctctcattaatgaatgctgggtcactcagacccc
25 (AseI restriction site is underlined)

30

Universal beta chain reverse primer
tagaaaccggtggccaggcacaccagtgtggc
(AgeI restriction site is underlined)

In the case of the TCR β chain a further PCR stitching was carried out to replace the amber stop codon in the CDR3 region with a codon encoding glutamic acid. When an

35

amber stop codon is suppressed in *E.coli*, a glutamine residue is normally introduced

instead of the translation being stopped. Therefore, when the amber codon-containing TCR is displayed on the surface of phage, it contains a glutamine residue in this position. However, when the TCR β -chain gene was transferred into the expression plasmid, a glutamic acid residue was used as an alternative to glutamine. The primers used for this PCR stitching were as follows.

5
YOL124 CTGCTCTGGTTCCGCACTC
YOL125 GAGTGCGGAACCAGAGCAG

10 The DNA sequence of the mutated soluble A6 TCR β chain was verified by automated sequencing (see Figure 14a for the mutated A6 TCR β chain DNA sequence and 14b for the amino acid sequence encoded thereby). Figure 14c shows the mutated A6 TCR β chain amino acid sequence without the glutamine to glutamic acid substitution, i.e. the sequence that was present in Clone 134 as isolated by phage-ELISA.

15 Theses A6 TCR α and β DNA sequences were then used to produce a soluble A6 TCR as described in WO 03/020763. Briefly, the two chains are expressed as inclusion bodies in separate *E.coli* cultures. The inclusion bodies are then isolated, de-natured and re-folded together *in vitro*.

20 *Example 10 – BIACore surface plasmon resonance characterisation of a high affinity A6 TCR binding to HLA-A2 Tax.*

25 A surface plasmon resonance biosensor (BIACore 3000TM) was used to analyse the binding of the high affinity clone 134 A6 TCR (See Figures 15a & 15b for the full DNA and amino acid sequences of the mutated TCR β chain respectively) to the HLA-A2 Tax ligand. This was facilitated by producing pMHC complexes (described below) which were immobilised to a streptavidin-coated binding surface in a semi-oriented fashion, allowing efficient testing of the binding of a soluble T-cell receptor 30 to up to four different pMHC (immobilised on separate flow cells) simultaneously. Manual injection of HLA complex allows the precise level of immobilised class I molecules to be manipulated easily.

Biotinylated class I HLA-A2 tax complexes were refolded *in vitro* from bacterially-expressed inclusion bodies containing the constituent subunit proteins and synthetic peptide, followed by purification and *in vitro* enzymatic biotinylation (O'Callaghan *et al.* (1999) *Anal. Biochem.* **266**: 9-15). HLA-heavy chain was expressed with a C-terminal biotinylation tag which replaces the transmembrane and cytoplasmic domains of the protein in an appropriate construct. Inclusion body expression levels of ~75 mg/litre bacterial culture were obtained. The HLA light-chain or β 2-microglobulin was also expressed as inclusion bodies in *E.coli* from an appropriate construct, at a level of ~500 mg/litre bacterial culture.

E. coli cells were lysed and inclusion bodies were purified to approximately 80% purity. Protein from inclusion bodies was denatured in 6 M guanidine-HCl, 50 mM Tris pH 8.1, 100 mM NaCl, 10 mM DTT, 10 mM EDTA, and was refolded at a concentration of 30 mg/litre heavy chain, 30 mg/litre β 2m into 0.4 M L-Arginine-HCl, 100 mM Tris pH 8.1, 3.7 mM cystamine, mM cysteamine, 4 mg/ml peptide (e.g. tax 11-19), by addition of a single pulse of denatured protein into refold buffer at < 5°C. Refolding was allowed to reach completion at 4°C for at least 1 hour.

Buffer was exchanged by dialysis in 10 volumes of 10 mM Tris pH 8.1. Two changes of buffer were necessary to reduce the ionic strength of the solution sufficiently. The protein solution was then filtered through a 1.5 μ m cellulose acetate filter and loaded onto a POROS 50HQ anion exchange column (8 ml bed volume). Protein was eluted with a linear 0-500 mM NaCl gradient. HLA-A2-peptide complex eluted at approximately 250 mM NaCl, and peak fractions were collected, a cocktail of protease inhibitors (Calbiochem) was added and the fractions were chilled on ice.

Biotinylation tagged HLA-A2 complexes were buffer exchanged into 10 mM Tris pH 8.1, 5 mM NaCl using a Pharmacia fast desalting column equilibrated in the same buffer. Immediately upon elution, the protein-containing fractions were chilled on ice and protease inhibitor cocktail (Calbiochem) was added. Biotinylation reagents were then added: 1 mM biotin, 5 mM ATP (buffered to pH 8), 7.5 mM MgCl₂, and 5 μ g/ml

BirA enzyme (purified according to O'Callaghan *et al.* (1999) *Anal. Biochem.* **266**: 9-15). The mixture was then allowed to incubate at room temperature overnight.

5 Biotinylated HLA-A2 complexes were purified using gel filtration chromatography. A Pharmacia Superdex 75 HR 10/30 column was pre-equilibrated with filtered PBS and 1 ml of the biotinylation reaction mixture was loaded and the column was developed with PBS at 0.5 ml/min. Biotinylated HLA-A2 complexes eluted as a single peak at approximately 15 ml. Fractions containing protein were pooled, chilled on ice, and protease inhibitor cocktail was added. Protein concentration was 10 determined using a Coomassie-binding assay (PerBio) and aliquots of biotinylated HLA-A2 complexes were stored frozen at -20°C. Streptavidin was immobilised by standard amine coupling methods.

15 The interactions between the high affinity A6 Tax TCR containing a novel inter-chain bond and the HLA-A2 Tax complex or an irrelevant HLA-A2 NY-ESO combination, the production of which is described above, were analysed on a BIACore 3000™ surface plasmon resonance (SPR) biosensor. SPR measures changes in refractive index expressed in response units (RU) near a sensor surface within a small flow cell, a principle that can be used to detect receptor ligand interactions and to analyse their 20 affinity and kinetic parameters. The probe flow cells were prepared by immobilising the individual HLA-A2 peptide complexes in separate flow cells via binding between the biotin cross linked onto β 2m and streptavidin which have been chemically cross linked to the activated surface of the flow cells. The assay was then performed by passing sTCR over the surfaces of the different flow cells at a constant flow rate, 25 measuring the SPR response in doing so. Initially, the specificity of the interaction was verified by passing soluble A6 TCR at a constant flow rate of 5 μ l min⁻¹ over four different surfaces; one coated with ~1000 RU of HLA-A2 Tax complex, the second coated with ~1000 RU of HLA-A2 NY-ESO complex, and two blank flow cells coated only with streptavidin (see Figure 15).

The increased affinity of the mutated soluble A6 TCR made calculation of the k_d for the interaction of this moiety with the HLA-A2 Tax complex difficult. However, the half-life ($t_{1/2}$) for the interaction was calculated to be 51.6 minutes (see Figure 16), which compares to a $t_{1/2}$ for the wild-type interaction of 7.2 seconds.

5

Example 11 – Production of vector encoding a soluble NY-ESO TCR containing a novel disulphide bond.

10 The β chain of the soluble A6 TCR prepared in Example 1 contains in the native sequence a BglII restriction site (AAGCTT) suitable for use as a ligation site.

15 PCR mutagenesis was carried as detailed below to introduce a BamH1 restriction site (GGATCC) into the α chain of soluble A6 TCR, 5' of the novel cysteine codon. The sequence described in Figure 2a was used as a template for this mutagenesis. The following primers were used:

| BamH1 |
5' -ATATCCAGAACCCgGATCCTGCCGTGTA-3'
5' -TACACGGCAGGAaTCcGGGTTCTGGATAT-3'

20

100 ng of plasmid was mixed with 5 μ l 10 mM dNTP, 25 μ l 10xPfu-buffer (Stratagene), 10 units Pfu polymerase (Stratagene) and the final volume was adjusted to 240 μ l with H₂O. 48 μ l of this mix was supplemented with primers diluted to give a final concentration of 0.2 μ M in 50 μ l final reaction volume. After an initial denaturation step of 30 seconds at 95°C, the reaction mixture was subjected to 15 rounds of denaturation (95°C, 30 sec.), annealing (55°C, 60 sec.), and elongation (73°C, 8 min.) in a Hybaid PCR express PCR machine. The product was then digested for 5 hours at 37°C with 10 units of DpnI restriction enzyme (New England Biolabs). 10 μ l of the digested reaction was transformed into competent XL1-Blue bacteria and 30 grown for 18 hours at 37°C. A single colony was picked and grown over night in 5 ml TYP + ampicillin (16 g/l Bacto-Tryptone, 16 g/l Yeast Extract, 5 g/l NaCl, 2.5 g/l

K₂HPO₄, 100 mg/l Ampicillin). Plasmid DNA was purified on a Qiagen mini-prep column according to the manufacturer's instructions and the sequence was verified by automated sequencing at the sequencing facility of Department of Biochemistry, Oxford University.

5

CDNA encoding NY-ESO TCR was isolated from T cells according to known techniques. CDNA encoding NY-ESO TCR was produced by treatment of the mRNA with reverse transcriptase.

10 In order to produce a vector encoding a soluble NY-ESO TCR incorporating a novel disulphide bond, A6 TCR plasmids containing the α chain BamHI and β chain BglII restriction sites were used as templates. The following primers were used:

15 | NdeI |
5' -GGAGATATACTATGCAGGAGGTGACACAG-3'
5' -TACACGGCAGGATCCGGTTCTGGATATT-3'
| BamHI |

20 | NdeI |
5' -GGAGATATACTATGGGTGTCACTCAGACC-3'
5' -CCCAAGCTTAGTCTGCCTACCCAGGCCTCGGC -3'
| BglII |

25 NY-ESO TCR α and β -chain constructs were obtained by PCR cloning as follows. PCR reactions were performed using the primers as shown above, and templates containing the native NY-ESO TCR chains. The PCR products were restriction digested with the relevant restriction enzymes, and cloned into pGMT7 to obtain expression plasmids. The sequence of the plasmid inserts were confirmed by
30 automated DNA sequencing. Figures 17a and 17b show the DNA sequence of the mutated NY-ESO TCR α and β chains respectively, and Figures 18a and 18b show the resulting amino acid sequences.

Example 12 - Construction of phage display vectors and cloning of DNA encoding NY-ESO TCR α and β chains into the phagemid vectors.

5 DNA encoding soluble NY-ESO TCR α and β chains incorporating novel cysteine codons to facilitate the formation of a non-native disulfide inter-chain bond, produced as described in Example 11 were incorporated into the phagemid vector pEX746 as follows.

10 The DNA encoding the two NY-ESO TCR chains were individually subjected to PCR in order to introduce cloning sites compatible with the pEX746 phagemid vector (containing DNA encoding A6 TCR clone 7) using the following primers:

For the NY-ESO TCR alpha chain

15 TRAV21
GCCGGCCATGGCCAAACAGGAGGTGACGCAGATTCCT
 YOL6
CTTCTAAAGAATTCTAATTAAACCTAGGTTATTAGGAACTTCTGGGCTG
 GGGAAAG

20 20 *For the NY-ESO TCR beta chain*

TRBV6-1/2/3/5/6/7/8/9
TCACAGCGCGCAGGCTGGTGTCACTCAGACCCAAA

25 RT1
 CGAGAGCCCCGTAGAACTGGACTTG

30 The molecular cloning methods for constructing the vectors are described in
 "Molecular cloning: A laboratory manual, by J. Sambrook and D. W. Russell".
 Primers listed in table-1 are used for construction of the vectors. A example of the
 PCR programme is 1 cycle of 94°C for 2 minutes, followed by 25 cycles of 94°C for 5
 seconds, 53°C for 5 seconds and 72°C for 90 seconds, followed by 1 cycles of 72°C
 for 10 minutes, and then hold at 4°C. The Expand-hifidelity-Taq-DNA-polymerase is
 35 purchased from Roche.

DNA encoding the clone 7 A6 TCR β chain was removed from pEX746 by digestion with restrictions enzymes BssHII and BglII. The correspondingly digested PCR DNA encoding the NY-ESO β chain was then substituted into the phagemid by ligation. The sequence of the cloning product was verified by automated sequencing.

5

Similarly, DNA encoding the clone 7 A6 TCR α chain was removed from pEX746 by digestion with restrictions enzymes NcoI and AvrII. The correspondingly digested PCR DNA encoding the NY-ESO α chain was then substituted into the phagemid already containing DNA encoding the NY-ESO TCR β chain by ligation. The

10

sequence of the cloning product was verified by automated sequencing.

Figure 19 details the DNA and amino acid sequence of the NY-ESO TCR α and β chain as well as surrounding relevant sequence incorporated in the phagemid (pEX746:NY-ESO) respectively. The sequence preceding the NcoI site (Figure 19) is the same as pEX746.

15

Example 13 – Expression of fusions of bacterial coat protein and heterodimeric NY-ESO TCR in E. coli.

20

Phage particles displaying the heterodimeric NY-ESO TCR containing a non-native disulfide inter-chain bond were prepared using methods described previously for the generation of phage particles displaying antibody scFvs (Li *et al*, 2000, Journal of Immunological Methods 236: 133-146) with the following modifications. *E. coli* TG 1 cells containing pEX746:NY-ESO phagemid (i.e. the phagemid encoding the soluble NY-ESO TCR α chain and an NY-ESO TCR β chain fused to the phage gIII protein produced as described in Example 12) were used to inoculate 10 ml of 2x TY

25

(containing 100 μ g/ml of ampicillin and 2% glucose), and then the culture was incubated with shaking at 37°C overnight (16 hours). 50 μ l of the overnight culture was used to inoculate 10 ml of 2x TY (containing 100 μ g/ml of ampicillin and 2% glucose), and then the culture was incubated with shaking at 37°C until OD_{600nm} = 0.8.

30

HYPERPHAGE Helper phage was added to the culture to the final concentration of 5 X 10⁹ pfu/ml. The culture was then incubated at 37°C stationary for thirty minutes and then with shaking at 200 rpm for further 30 minutes. The medium of above culture

was then made up to 50 ml with 2x TY (containing 100 μ g/ml of ampicillin and 25 μ g/ml of kanamycin), the culture was then incubated at 25°C with shaking at 250 rpm for 36 to 48 hours. The culture was then centrifuged at 4°C for 30 minutes at 4000 rpm. The supernatant was filtrated through a 0.45 μ m syringe filter and stored at 4°C 5 for further concentration. The supernatant was then concentrated by PEG precipitation and re-suspended in PBS at 10% of the original stored volume.

Example 14 – Detection of functional heterodimeric NY-ESO TCR containing a non-native disulfide inter-chain bond on filamentous phage particles

10 The presence of functional (HLA-A2-NY-ESO binding) NY-ESO TCR displayed on the phage particles in the concentrated suspension prepared in Example 13 was detected using the phage ELISA methods described in Example 4. Figure 20 shows the specific binding of phage particles displaying the NY-ESO TCR to HLA-A2-NY-ESO 15 in a phage ELISA assay.

Example 15 - Construction of plasmids for cellular expression of HLA-DRA genes.

20 DNA sequences encoding the extracellular portion of HLA-DRA chains are amplified from cDNA isolated from the blood of a healthy human subject, using the polymerase chain reaction (PCR), with synthetic DNA primer pairs that are designed to include a Bgl II restriction site.

25 PCR mutagenesis is then used to add DNA encoding the Fos leucine zipper to the 3' end of the amplified sequencence.

DNA manipulations and cloning described above are carried out as described in Sambrook, J *et al*, (1989). Molecular Cloning - A Laboratory Manual. Second Edition. Cold Spring Harbor Laboratory Press, USA.

Figure 21 provides the DNA sequence of the HLA-DR β chain ready for insertion into the bi-cistronic expression vector. This figure indicates the position of the codons encoding the Fos leucine zipper peptide and the biotinylation tag.

5 Amino acid numbering is based on the mouse sequence (Kabat, 1991, Sequences of Proteins of Immunological Interest, 5th edition, US Dept of Health & Human Services, Public Health Service, NIH, Bethesda, MD 1-1137)

10 This DNA sequence is then inserted into a bi-cistronic baculovirus vector pAcAB3 (See Figure 22 for the sequence of this vector) along with DNA encoding the corresponding Class II HLA β chain for expression in Sf9 insect cells. This vector can be used to express any Class II HLA-peptide complex in insect cells.

15 *Example 16. Construction of plasmids for cellular expression of HLA-DRB wild type and mutant genes.*

20 DNA sequences encoding the extracellular portion of HLA-DRB chains are amplified from cDNA isolated from the blood of a healthy human subject, using the polymerase chain reaction (PCR), with synthetic DNA primer pairs that are designed to include a BamH1 restriction site.

PCR mutagenesis is then used to add DNA encoding the Jun leucine zipper to the 3' end of the amplified sequence and DNA encoding the Flu HA peptide loaded by the HLA-DR1 molecule to the 5' end of the sequence.

25 DNA manipulations and cloning described above are carried out as described in Sambrook, J *et al*, (1989). Molecular Cloning - A Laboratory Manual. Second Edition. Cold Spring Harbor Laboratory Press, USA.

Figure 23 provides the DNA sequence of the HLA-DR β chain ready for insertion into the bi-cistronic expression vector. This figure indicates the position of the codons encoding the Jun leucine zipper peptide and the Flu HA peptide.

5 Amino acid numbering is based on the mouse sequence (Kabat, 1991, Sequences of Proteins of Immunological Interest, 5th edition, US Dept of Health & Human Services, Public Health Service, NIH, Bethesda, MD 1-1137)

10 This DNA sequence is then inserted into a bi-cistronic baculovirus vector pAcAB3 (See Figure 22 for the sequence of this vector) along with DNA encoding the corresponding Class II α chain for expression in Sf9 insect cells. This vector can be used to express any Class II HLA-peptide complex in insect cells.

15 *Example 17 Expression and refolding of Class II HLA-DR1- Flu HA complexes*

Class II MHC expression is carried out using the bi-cistronic expression vectors produced as described in Examples 15 and 16 containing the Class II HLA-DR1 α and β chains and the Flu HA peptide. The expression and purification methods used are as 20 described in (Gauthier (1998) PNAS USA 95 p11828-11833). Briefly, soluble HLA-DR1 is expressed in the baculovirus system by replacing the hydrophobic transmembrane regions and cytoplasmic segments of DR α and β chains with leucine zipper dimerization domains from the transcription factors Fos and Jun. In the expression construct, the required Class MHC-loaded Flu HA peptide sequence is 25 covalently linked to the N terminus of the mature DR β chain and the DR α chain contains a biotinylation tag sequence to facilitate bifunctional ligand formation utilizing the biotin / streptavidin multimerisation methodology. The recombinant protein is secreted by Sf9 cells infected with the recombinant baculovirus, and purified by affinity chromatography. The protein is further purified by anion-exchange HPLC.

30

Example 18 –Construction of Class I soluble peptide-HLA molecules

In order to investigate further the specificity of the high affinity A6 TCR clone 134 the following soluble class I peptide-HLA molecules were produced:

5

HLA-A2 – peptide (LLGRNSFEV)

HLA-A2 – peptide (KLVALGINAV)

HLA-A2 – peptide (LLGDLFGV)

HLA-B8 - peptide (FLRGRAYGL)

10 HLA-B27 – peptide (HRCQAIRKK)

HLA - Cw6 – peptide (YRSGIIAVV)

HLA-A24 – peptide (VYGFVRACL)

HLA-A2 – peptide (ILAKFLHWL)

HLA-A2 – peptide (LTLGEFLKL)

15 HLA-A2 – peptide (GILGFVFTL)

HLA-A2 – peptide (SLYNTVATL)

These soluble peptide-HLAs were produced using the methods described in Example 10.

20

Example 19 – BIAcore surface plasmon resonance measurement of the specificity of a high affinity A6 TCR binding to peptide-HLA.

A surface plasmon resonance biosensor (BIAcore 3000TM) was used to analyse the binding specificity of the high affinity clone 134 A6 TCR. (See Figures 15a & 15b for the full DNA and amino acid sequences of the mutated TCR β chain respectively) This was carried out using the Class II HLA-DR1-peptide, produced as described in Examples 15 –17, and the Class I peptide-HLA complexes listed in Example 18, produced using the methods detailed in Example 10. The following table lists the peptide-HLA complexes utilised:

1. HLA-A2 – peptide (LLGRNSFEV)
2. HLA-A2 – peptide (KLVALGINAV)
3. HLA-A2 – peptide (LLGDLFGV)
4. HLA-B8 - peptide (FLRGRAYGL)
5. HLA-B27 – peptide (HRCQAIRKK)
6. HLA - Cw6 – peptide (YRSGIIAVV)
7. HLA-A24 – peptide (VYGFVRACL)
8. HLA-A2 – peptide (ILAKFLHWL)
9. HLA-A2 – peptide (LTLGEFLKL)
10. HLA-DR1- peptide (PKYVKQNTLKLA)
11. HLA-A2 – peptide (GILGFVFTL)
12. HLA-A2 – peptide (SLYNTVATL)

15 The above peptide HLAs were immobilised to streptavidin-coated binding surfaces in
of the flow cells of a BIACore 3000TM in a semi-oriented fashion.

20 The BIACore 3000TM allows testing of the binding of the soluble T-cell receptor to up
to four different pMHC (immobilised on separate flow cells) simultaneously. For this
experiment three different HLA-peptides were immobilised in flowcells 2-4 and
flowcell 1 was left blank as a control. Manual injection of HLA-peptide complexes
allowed the precise level of immobilised molecules to be manipulated.

25 After the ability of the high affinity A6 TCR clone 134 to bind to the first 3 HLA-
peptide complexes in the above list had been assessed the next three were immobilised
onto these flowcells directly on top of the previous ones. This process was continued
until the binding of the high affinity A6 TCR clone 134 to all 12 HLA-peptide
complexes had been assessed.

30 Ten injections of 5 μ l of the high affinity A6 TCR clone 134 were passed over each
flowcell at at 5 μ l/min at concentrations ranging from 4.1 ng/ml to 2.1 mg/ml. (See
Figures 24-28)

As a final control the high affinity A6 TCR clone 134 was passed over a flowcell containing immobilised HLA-A2 Tax (LLFGYPVYV), the cognate ligand for this TCR.

5

Specific binding of the high affinity A6 TCR clone 134 was only noted to its cognate ligand. (HLA-A2 Tax (LLFGYPVYV)) These data further demonstrate the specificity of the high affinity A6 TCR clone 134.

Claims:

1. A proteinaceous particle displaying on its surface a T-cell receptor (TCR), characterised in that

5

(i) the proteinaceous particle is a ribosome and the TCR is a single chain TCR (scTCR) polypeptide, or

10 (ii) the proteinaceous particle is a phage particle or a cell surface protein or polypeptide and the TCR is a human scTCR or a human dimeric T-cell receptor (dTCR) polypeptide pair, or

15 (iii) the proteinaceous particle is a phage particle or a cell surface protein or polypeptide and the TCR is a non-human dTCR polypeptide pair, or

20 (iv) the proteinaceous particle is a phage particle or a cell surface protein or polypeptide and the TCR is a scTCR polypeptide comprising TCR amino acid sequences corresponding to extracellular constant and variable region sequences present in native TCR chains and a linker sequence, the latter linking a variable region sequence corresponding to that of one chain of a native TCR to a constant region sequence corresponding to a constant region sequence of another native TCR chain, and a disulfide bond which has no equivalent in native T cell receptors links residues of the constant region sequences.

25

2. A proteinaceous particle, displaying on its surface a dimeric T-cell receptor (dTCR) polypeptide pair, or a single chain T-cell receptor (scTCR) polypeptide wherein

30 the dTCR polypeptide pair is constituted by TCR amino acid sequences corresponding to extracellular constant and variable region sequences present in native TCR chains,

and the scTCR is constituted by TCR amino acid sequences corresponding to extracellular constant and variable region sequences present in native TCR chains and a linker sequence, the latter linking a variable region sequence corresponding to that of one chain of a native TCR to a constant region sequence corresponding to a constant region sequence of another native TCR chain;

5 the variable region sequences of the dTCR polypeptide pair or scTCR polypeptide are mutually orientated substantially as in native TCRs; and

10 in the case of the scTCR polypeptide a disulfide bond which has no equivalent in native T cell receptors links residues of the polypeptide.

3. A proteinaceous particle as claimed in claim 1 or claim 2, which is a phage particle.

15 4. A proteinaceous particle as claimed in claim 1 or claim 2, which is a cell surface protein or polypeptide.

20 5. A proteinaceous particle as claimed in claim 1 or claim 2, which is a ribosome.

25 6. A proteinaceous particle as claimed in any of the preceding claims wherein the C-terminus of one member of the dTCR polypeptide pair, or the C-terminus of the scTCR polypeptide, is linked by a peptide bond to a surface exposed residue of the proteinaceous particle.

30 7. A proteinaceous particle as claimed in any of claims 1 to 4 wherein the C-terminus of one member of the dTCR polypeptide pair, or the C-terminus of the scTCR polypeptide, is linked by a disulfide bond to a surface exposed cysteine residue of the proteinaceous particle.

8. A proteinaceous particle as claimed in any of the preceding claims wherein an scTCR polypeptide is displayed which comprises

5 a first segment constituted by an amino acid sequence corresponding to a TCR α or δ chain variable region

10 a second segment constituted by an amino acid sequence corresponding to a TCR β or γ chain variable region sequence fused to the N terminus of an amino acid sequence corresponding to a TCR β chain constant region extracellular sequence, and

15 a linker sequence linking the C terminus of the first segment to the N terminus of the second segment.

20 9. A proteinaceous particle as claimed in any of claims 1 to 7 wherein an scTCR polypeptide is displayed which comprises

25 a first segment constituted by an amino acid sequence corresponding to a TCR β or γ chain variable region

30 a second segment constituted by an amino acid sequence corresponding to a TCR α or δ chain variable region sequence fused to the N terminus of an amino acid sequence corresponding to a TCR α chain constant region extracellular sequence, and

35 a linker sequence linking the C terminus of the first segment to the N terminus of the second segment.

40 10. A proteinaceous particle as claimed in any of claims 1 to 7 wherein a scTCR polypeptide is displayed which has

a first segment constituted by an amino acid sequence corresponding to a TCR α or δ chain variable region sequence fused to the N terminus of an amino acid sequence corresponding to a TCR α chain constant region extracellular sequence,

5 a second segment constituted by an amino acid sequence corresponding to a TCR β or γ chain variable region fused to the N terminus of an amino acid sequence corresponding to TCR β chain constant region extracellular sequence,

10 a linker sequence linking the C terminus of the first segment to the N terminus of the second segment, or vice versa, and

a disulfide bond between the first and second chains, said disulfide bond being one which has no equivalent in native $\alpha\beta$ or $\gamma\delta$ T cell receptors,

15 the length of the linker sequence and the position of the disulfide bond being such that the variable region sequences of the first and second segments are mutually orientated substantially as in native $\alpha\beta$ or $\gamma\delta$ T cell receptors.

11. A proteinaceous particle as claimed in claim 10 wherein the linker sequence 20 has the formula -P-AA-P- wherein P is proline and AA represents an amino acid sequence wherein the amino acids are glycine and serine.

12. A proteinaceous particle as claimed in claim 10 or claim 11 wherein the linker sequence links the C terminus of the first segment to the N terminus of the second 25 segment.

13. A proteinaceous particle as claimed in claim 12 wherein the linker sequence consists of from 26 to 41 amino acids.

30 14. A proteinaceous particle as claimed in claim 13 wherein the linker sequence consists of 29, 30, 31 or 32 amino acids.

15. A proteinaceous particle as claimed in claim 13 wherein the linker sequence consists of 33, 34, 35 or 36 amino acids.

5 16. A proteinaceous particle as claimed in claim 13 wherein the linker sequence has the formula -PGGG-(SGGGG)₅-P- wherein P is proline, G is glycine and S is serine.

10 17. A proteinaceous particle as claimed in claim 13 wherein the linker sequence has the formula -PGGG-(SGGGG)₆-P- wherein P is proline, G is glycine and S is serine.

18. A proteinaceous particle as claimed in any of claims 1 to 4, 6 or 7 wherein a dTCR polypeptide pair is displayed which is constituted by

15 a first polypeptide wherein a sequence corresponding to a TCR α or δ chain variable region sequence is fused to the N terminus of a sequence corresponding to a TCR α chain constant region extracellular sequence, and

20 a second polypeptide wherein a sequence corresponding to a TCR β or γ chain variable region sequence fused to the N terminus a sequence corresponding to a TCR β chain constant region extracellular sequence,

25 the first and second polypeptides being linked by a disulfide bond which has no equivalent in native $\alpha\beta$ or $\gamma\delta$ T cell receptors.

19. A proteinaceous particle as claimed in any preceding claim wherein the displayed dTCR polypeptide pair or scTCR polypeptide have amino acid sequences corresponding to $\alpha\beta$ TCR extracellular constant and variable region sequences.

20. A proteinaceous particle as claimed in any of claims 1 to 18 wherein the displayed dTCR polypeptide pair or scTCR polypeptide have amino acid sequences corresponding to extracellular $\alpha\beta$ TCR constant region sequences and $\gamma\delta$ TCR variable region sequences.

5

21. A proteinaceous particle as claimed in any preceding claim wherein the displayed dTCR polypeptide pair or scTCR polypeptide have amino acid sequences corresponding to non-human extracellular $\alpha\beta$ TCR constant region sequences and human TCR variable region sequences.

10

22. A proteinaceous particle as claimed in any of the preceding claims wherein an amino acid sequence of one member of the displayed dTCR polypeptide pair, or an amino acid sequence of the displayed scTCR, corresponds to a native TCR extracellular constant chain Ig domain sequence.

15

23. A proteinaceous particle as claimed in any of the preceding claims wherein the displayed dTCR polypeptide pair or displayed scTCR, includes sequences corresponding to native TCR extracellular constant chain Ig domain sequences.

20

24. A proteinaceous particle as claimed in claim 23 wherein a disulfide bond links amino acid residues of the said constant chain Ig domain sequences, which disulfide bond has no equivalent in native TCRs.

25

25. A proteinaceous particle as claimed in claim 24 wherein the said disulfide bond is between cysteine residues corresponding to amino acid residues whose β carbon atoms are less than 0.6 nm apart in native TCRs.

30

26. A proteinaceous particle as claimed in claim 24 wherein the said disulfide bond is between cysteine residues substituted for Thr 48 of exon 1 of TRAC*01 and Ser 57 of exon 1 of TRBC1*01 or TRBC2*01 or the non-human equivalent thereof.

27. A proteinaceous particle as claimed in claim 24 wherein the said disulfide bond is between cysteine residues substituted for Thr 45 of exon 1 of TRAC*01 and Ser 77 of exon 1 of TRBC1*01 or TRBC2*01 or the non-human equivalent thereof.

5 28. A proteinaceous particle as claimed in claim 24 wherein the said disulfide bond is between cysteine residues substituted for Tyr 10 of exon 1 of TRAC*01 and Ser 17 of exon 1 of TRBC1*01 or TRBC2*01 or the non-human equivalent thereof.

10 29. A proteinaceous particle as claimed in claim 24 wherein the said disulfide bond is between cysteine residues substituted for Thr 45 of exon 1 of TRAC*01 and Asp 59 of exon 1 of TRBC1*01 or TRBC2*01 or the non-human equivalent thereof.

15 30. A proteinaceous particle as claimed in claim 24 wherein the said disulfide bond is between cysteine residues substituted for Ser 15 of exon 1 of TRAC*01 and Glu 15 of exon 1 of TRBC1*01 or TRBC2*01 or the non-human equivalent thereof.

20 31. A proteinaceous particle as claimed in any of claims 23 to 30 wherein the sequences corresponding to native TCR extracellular constant chain Ig domain sequences are truncated at their C-termini relative to said native sequences such that the cysteine residues which form the native interchain disulphide bond are excluded.

25 32. A proteinaceous particle as claimed in any of claims 23 to 30 wherein in the sequences corresponding to native TCR extracellular constant chain Ig domain sequences the cysteine residues which form the native interchain disulphide bond are substituted by non-cysteine residues.

33. A proteinaceous particle as claimed in claim 32 wherein the cysteine residues which form the native interchain disulfide bond are substituted by serine or alanine.

34. A proteinaceous particle as claimed in any of the preceding claims wherein in the displayed dTCR or scTCR there is no unpaired cysteine residue corresponding an unpaired cysteine residue present in a native TCR.

5 35. A proteinaceous particle as claimed in any of claims 23 to 34 wherein the sequences corresponding to native TCR extracellular constant chain Ig domain sequences are truncated N-terminal to residues corresponding to those which form the non-native interchain disulphide bond.

10 36. A diverse library of dTCR polypeptide pairs or scTCR polypeptides displayed on proteinaceous particles said dTCR polypeptide pairs or scTCR polypeptides having the structural features defined in any of claims 8 to 35.

15 37. A diverse library as claimed in claim 36 wherein the diversity resides in the variable region(s) of the dTCR or scTCR polypeptides.

38. A diverse library as claimed in claim 36 wherein the diversity resides in one or more of the complementarity determining regions of the variable region(s) of the dTCR or scTCR polypeptides.

20 39. A diverse library as claimed in any of claims 36 to 38 wherein the dTCR or scTCR polypeptides are displayed on phage particles.

25 40. Nucleic acid encoding (a) one chain of a dTCR polypeptide pair and (b) the other chain of a dTCR polypeptide pair fused to a nucleic acid sequence encoding a particle forming protein, or nucleic acid encoding a scTCR polypeptide fused to a nucleic acid sequence encoding a particle forming protein, the dTCR pair or scTCR having the structural features defined in any of claims 8 to 35.

30 41. An expression vector comprising nucleic acid as claimed in claim 40.

42. An expression vector as claimed in claim 41 which is a phagemid or phage genome vector.

43. A phagemid or phage genome vector as claimed in claim 42 wherein the 5 nucleic acid sequence(s) which encode the particle-forming protein is (are) derived from a filamentous phage.

44. A phagemid or phage genome vector as claimed in claim 43 wherein the said nucleic acid sequence(s) encode(s) bacteriophage gIII or gVIII coat proteins.

10 45. An expression vector as claimed in any of claims 41 to 44 containing a sequence or sequences which limit constitutively or inducibly the amount of TCR polypeptide expressed by the vector to a desired level.

15 46. An expression vector as claimed in claim 45 wherein the said sequence(s) is (are) weak promoter sequence(s).

47. An expression vector as claimed in claim 45 wherein the said sequence(s) is (are) mutated ribosome binding site(s).

20 48. An expression vector as claimed in claim 45 wherein the said sequence(s) is (are) miss-sense suppressor stop codon(s).

49. An expression vector as claimed in claim 45 wherein the said sequence(s) is (are) mutated start codon(s).

25 50. An expression vector as claimed in claim 45 wherein the said sequence(s) contain(s) a number of codons less preferred by the expression system being utilised.

30

51. A host cell comprising nucleic acid as claimed in claim 40, or an expression vector as claimed in any of claims 41 to 50.

52. A host cell harbouring a phagemid expression vector as claimed in any of claims 42 to 50, and a helper phage.

53. A method for the identification of TCRs with a specific characteristic, said method comprising subjecting a diverse library of TCRs displayed on proteinaceous particles as claimed in any of claims 36 to 39 to an assay which measures said 10 characteristic, identifying those proteinaceous particles which display a TCR with the desired characteristic and isolating these proteinaceous particles.

54. A method as claimed in claim 53 wherein the specific characteristic is increased affinity for a TCR ligand.

15 55. A method for detecting TCR ligand complexes, which comprises:
(i) providing a TCR-displaying proteinaceous particle as claimed in any of claims 1 to 39;
(ii) contacting said TCR-displaying proteinaceous particle with a putative 20 ligand complex; and
(iii) detecting binding of the said TCR-displaying proteinaceous particle to the putative ligand complexes.

56 56. A method as claimed in claim 55 wherein the putative TCR ligand complexes 25 are peptide-MHC complexes.

57. A method of identifying an inhibitor of the interaction between a TCR- 30 displaying proteinaceous particle as claimed in any one of claims 1 to 39, and a TCR-binding ligand comprising contacting the TCR-displaying proteinaceous particle with a TCR-binding ligand, in the presence of and in the absence of a test compound, and determining whether the presence of the test compound reduces binding of the TCR-

displaying proteinaceous particle to the TCR-binding ligand, such reduction being taken as identifying an inhibitor.

5 58. A TCR specific for a given TCR ligand, which (i) has the structural features defined in any of claims 8 to 35, (ii) is mutated in the variable region(s) relative to the native TCR specific for said TCR ligand and which (iii) has a Kd for the said TCR ligand less than that of the native TCR.

10 59. A TCR specific for a given TCR ligand, which (i) has the structural features defined in any of claims 8 to 35, (ii) is mutated in the variable region(s) relative to the native TCR specific for said TCR ligand and which (iii) has a Kd for the said TCR ligand less than that of the native TCR as measured by Surface Plasmon Resonance.

15 60. A TCR specific for a given TCR ligand, which (i) has the structural features defined in any of claims 8 to 35, (ii) is mutated in the variable region(s) relative to the native TCR specific for said TCR ligand and which (iii) has an off-rate (k_{off}) for the said TCR ligand less than that of the native TCR

20 61. A TCR specific for a given TCR ligand, which (i) has the structural features defined in any of claims 8 to 35, (ii) is mutated in the variable region(s) relative to the native TCR specific for said TCR ligand and which (iii) has an off-rate (k_{off}) for the said TCR ligand less than that of the native TCR as measured by Surface Plasmon Resonance.

25 62. A dimeric TCR as claimed in any of claims 58 to 61 which has the structural features of an $\alpha\beta$ heterodimeric TCR defined in any of claims 18 to 35.

30 63. A TCR as claimed in any of claims 58 to 62 which is mutated relative to the native TCR in at least one complementarity determining region.

64. A TCR as claimed in any of claims 58 to 63 which is specific for a given MHC type or types.

65. A TCR as claimed in any of claims 58 to 63 which is specific for a given
5 pMHC.

66. A TCR as claimed in any of claims 58 to 63 or 65 which is specific for the HLA-A2 Tax peptide (LLFGYPVYV) complex.

10 67. A TCR as claimed in any of claims 58 to 66 associated with a therapeutic or imaging compound.

68. A TCR as claimed in any of claims 58 to 66 associated with a cytotoxic compound.

15 69. A TCR as claimed in claim 68 wherein the TCR is specific for the HLA-A2 Tax peptide (LLFGYPVYV) complex.

70. A method of treatment of HTLV-1 infection comprising administering to a
20 subject suffering such infection an effective amount of a TCR as claimed in claim 66 or claim 68.

71. The use of a TCR as claimed in claim 66 or claim 68 in the preparation of a composition for the treatment of HTLV-1 infection.

Figure 1a

atgcagaaggaagtggagcagaactctggacccctcagtgttccagagggagccatt
gcctctctcaactgcacttacagtgaccgagggttccagtccttcttctggtacaga
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gaagatggaaggttacagcacagctcaataaagccagccagtatgttctgtc
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Figure 1b

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Figure 2a

MQ
K₁EVEQNSGPL SVPEGAIASL NCTYSDRGSQ SFFWYRQYSG KSPELIMSIY
SNGDKEDGRF TAQLNKASQY VSLLIRDSQP SDSATYLCAV TTDSWGKLQF
GAGTQVVVTP DIQNPDPAVY QLRDSKSSDK SVCLFTDFDS QTNVSQSKDS
DVYITDKCVL DMRSMDFKSN SAVAWSNKSD FACANAFNNS IIPEDTFFPS
PESS*

Figure 2b

M
N₁AGVTQTPKF QVLKTGQSMT LQCAQDMNHE YMSWYRQDPG MGLRLIHYSV
GAGITDQGEV PNGYNVSRST TEDFPLRLS AAPSQTSVYF CASRPGLAGG
RPEQYFGPGT RLTVTEDLKN VFPPEVAVFE PSEAEISHTQ KATLVCLATG
FYPDHVELSW WVNGKEVHSG VCTDPQPLKE QPALNDSRYA LSSRLRVSAT
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Figure 3

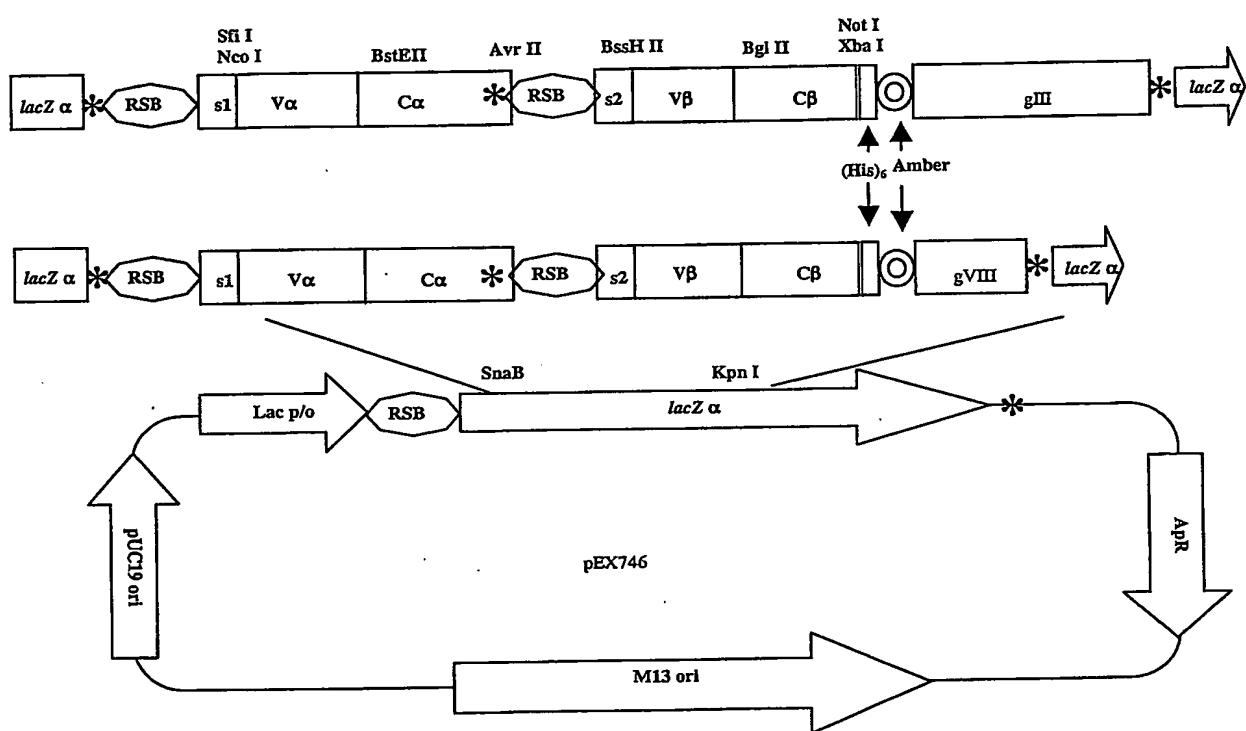
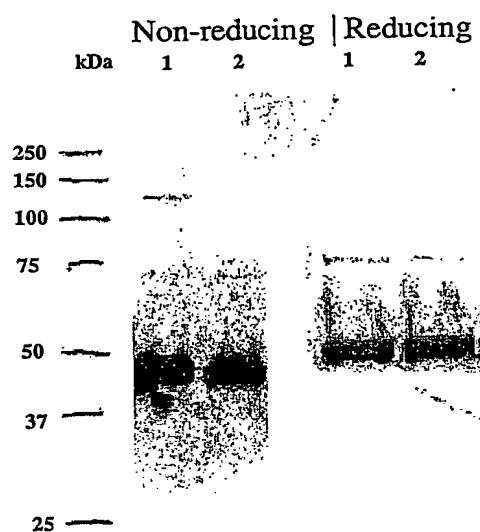


Figure 4

1 gttaactacg tcaggtggca ctttcgggg aatgtgcgc ggaaccctta tttgtttatt
 61 tttctaaata cattcaaata tttatccgct catgagacaa taaccctgat aaatgcttca
 121 ataatattga aaaaggaga gtatgagtat tcaacatttc cgtgtcgccc ttatccctt
 181 tttgcggca tttgccttc ctgttttgc tcacccagaa acgctggta aagtaaaaga
 241 tgctgaagat cagttgggtg cacgagtggg ttacatcgaa ctggatctca acagcggtaa
 301 gatcctttag agtttcgccc cccaagaacg ttctccaatg atgagcaattt taaagttct
 361 gctatgtggc gcggtaattat cccgtgtga cggccggca gagaactcg gtcggccat
 421 acactattct cagaatgact tggttgagta ctaccaggc acagaaaagc atcttacgga
 481 tggcatgaca gtaagagaat tatgcagtgc tgccataacc atgagtata acactgcggc
 541 caacttactt ctgacaacga tcggaggacc gaaggagcta accgctttt tgacacaacat
 601 ggggatcat gtaactcgcc ttgatcggtt ggaaccggag ctgaatgaag ccataccaaa
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 781 agttcagga ccaactctgc gctcgccct tccggctggc tggtttattt ctgataaattc
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 3061 cagtgtgtg gcctggagca acaaatctga ctttgcattgt gcaaaacgcct tcaacaacag
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 4561 atgacgctta ctggAACGGT aaattcagag actgcgttt ccattctggc ttatgagg
 4621 atccattcgt ttgtgaatat caaggccat cgtctgaccc gcctcaaccc cctgtcaatg
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 4801 attttgatta tgaaaagatg gcaaaacgta ataagggggc tatgaccgaa aatgccgatg
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Figure 5



7/34

Figure 6

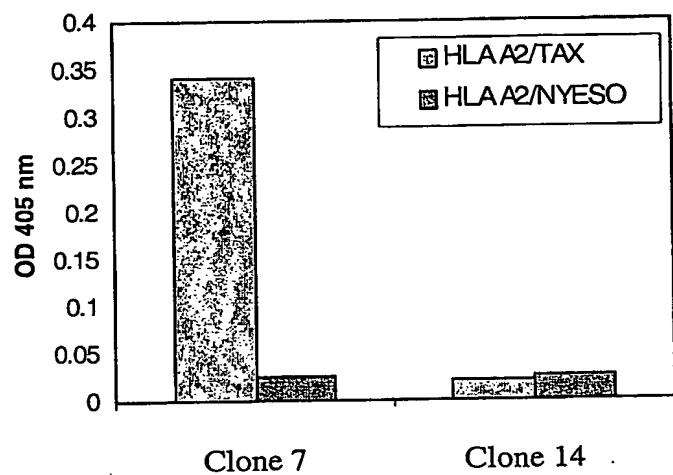


Figure 7a

Schematic diagram of the A6 scTCR-C-Kappa ribosome display construct

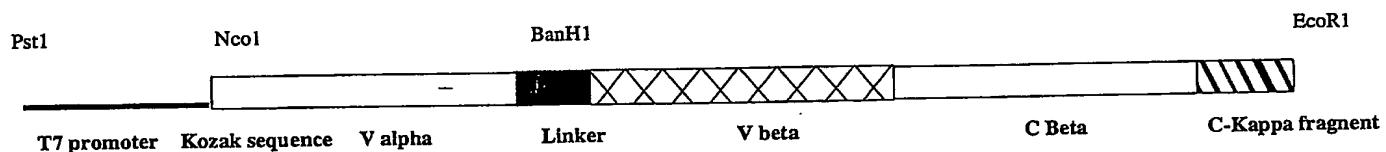


Figure 7b

TCGTCCCTGG GTCCAACACC AGTGGCCACC TCCGCCAAGT CCGCCTCCAC
 BamHI

1251 GATCCGGCGG TGGCGGGTCG AACGCTGGTG TCACTCAGAC CCCAAAATTC
 CTAGGCCGCC ACCGCCAGC TTGCGACCAC AGTGAGTCTG GGGTTTTAAG
 PstI

1251 CAGGTCCCTGA AGACAGGACA GAGCATGACA CTGCAGTGTG CCCAGGATAT
 GTCCAGGACT TCTGTCCTGT CTCGACTGT GACGTCACAC GGGTCCCTATA
 N H E Y M S W Y R Q D P G M G L R

1251 GAACCATGAA TACATGTCCT GGTATCGACA AGACCCAGGC ATGGGGCTGA
 CTTGGTACTT ATGTACAGGA CCATAGCTGT TCTGGGTCCG TACCCCGACT
 L I H Y S V G A G I T D Q G E V

1251 GGCTGATTCA TTACTCAGTT GGTGCTGGTA TCACTGACCA AGGAGAAGTC
 CCGACTAAGT AATGAGTCAA CCACGACCAT AGTGAAGTGGT TCCTCTTCAG
 P N G Y N V S R S T T E D F P L R

1251 CCCAATGGCT ACAATGTCCTC CAGATCAACCC ACAGAGGATT TCCCGCTCAG
 GGGTTACCGA TGTACAGAG GTCTAGTGG TGTCTCCCAA AGGGCGAGTC
 L L S A A P S Q T S V Y F C A S R

1251 GCTGCTGTCG GCTGCTCCCT CCCAGACATC TGTGTACTTC TGTGCCAGCA
 CGACGACAGC CGACGAGGGA GGGTCTGTAG ACACATGAAG ACACGGTCGT
 ScaI

1251 GGCCGGGACT AGCGGGAGGG CGACCAGAGC AGTACTTCGG GCCGGGCACC
 CCGGCCCTGA TCGCCCTCCC GCTGGTCTCG TCATGAAGCC CGGCCCGTGG
 R L T V T E D L K N V F P P E V A

1251 AGGCTCACGG TCACAGAGGA CCTGAAAAAC GTGTTCCAC CCGAGGTCGC
 TCCGAGTGCC AGTGTCTCCT GGACTTTTG CACAAGGGTG GGCTCCAGCG
 BglII

1251 TGTGTTGAG CCATCAGAAG CAGAGATCTC CCACACCAA AAGGCCACAC
 ACACAAACTC GGTAGTCTTC GTCTCTAGAG GGTGTGGT TTCCGGTGTG
 V C L A T G F Y P D H V E L S W

1251 TGGTGTGCCT GGCCACAGGC TTCTACCCCG ACCACGTGGA GCTGAGCTGG
 ACCACACGGA CCGGTGTCCG AAGATGGGGC TGGTGCACCT CGACTCGACC
 ApaLI

1251 TGGGTGAATG GGAAGGAGGT GCACAGTGGG GTCAGCACAG ACCCGCAGCC
 ACCCACTTAC CCTCCCTCCA CGTGTACCC CAGTCGTGTC TGGGCGTCGG
 L K E Q P A L N D S R Y A L S S R

1251 CCTCAAGGAG CAGCCCGGCC TCAATGACTC CAGATACGCT CTGAGCAGCC
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 Bsu36I

1251 GCCTGAGGGT CTCGGCCACC TTCTGGCAGG ACCCCCCCAA CCACCTCCGC
 CGGACTCCCA GAGCCGGTGG AAGACCGTCC TGGGGCGTT GGTGAAGGCG
 C Q V Q F Y G L S E N D E W T Q D

1251 TGTCAGTCC AGTTCTACGG GCTCTCGGAG AATGACGAGT GGACCCAGGA
ACAGTTCAAGG TCAAGATGCC CGAGAGCCTC TTACTGCTCA CCTGGGTCT
StuI

· R A K P V T Q I V S A E A W G R A ·

1251 TAGGGCCAAA CCCGTCACCC AGATCGTCAG CGCCGAGGCC TGGGGTAGAG
ATCCCGGTTT GGGCAGTGGG TCTAGCAGTC CGGGCTCCGG ACCCCATCTC
· D G G G G S L S S T L T L S K A ·

1251 CAGACGGTGG AGGGGTTCA CTCAGCAGCA CCCTGACGCT GAGCAAAGCA
GTCTGCCACC TCCGCCAAGT GAGTCGTCGT GGGACTGCGA CTCGTTTCGT
· D Y E K H K V Y A C E V T H Q G L ·

1251 GACTACGGAGA AACACAAAGT CTACGCCCTGC GAAGTCACCC ATCAGGGCCT
CTGATGCTCT TTGTGTTTCA GATGCGGACG CTTCAAGTGGG TAGTCCCGGA
EcoRI

· S S P V T K S F N R G E S ·

1251 GAGTTCCGCC GTCACAAAGA GCTTCAACCG CGGAGAGTC TAAGAAATTCT
CTCAAGCGGG CAGTGTTCCT CGAAAGTTGGC GCCTCTCAGT ATTCTTAAGA

1251 CAG
GTC

Figure 8

pUC19-T7 sequence

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 71 tccaccgtga aaagccctt tacacgcgc ttggggataaa acaaataaaa agatttatgt aagtttatac
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 491 cttaactgaac caactcatga gtggtcgtg tctttcgtt gaatgcgtac cgtactgtca ttctttaat
 561 acgttcacac ggtattggta ctcactatt tgacgcgggt tgaatgaaga ctgttgcgt tag ctcctggct
 631 tcctcgattt gcgaaaaaaaat ttgttgcattt cccttagtaca ttgagcggaa ctgcaccc ttggcctcga
 701 cttaacttcgg tattgttgc tgctcgact gtgggtctac ggacatcggtt accgttggtaa caacgcgtt
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 2031 cgcgcacccg gtcgttttttgcgtt gtcgcacca aacaaacggc ctatgttgcgtt atggttggaa
 2101 tgcgttgcgtt aacttcgcgtt gtcgttttttgcgtt gtcgcacca aacaaacggc ctatgttgcgtt atggttggaa
 2171 caacacaccc ttcgttttttgcgtt gtcgcacca aacaaacggc ctatgttgcgtt atggttggaa
 2241 gtcgttgcgtt gtcgttttttgcgtt gtcgcacca aacaaacggc ctatgttgcgtt atggttggaa
 2311 gcaatgggggg gtcgttttttgcgtt gtcgcacca aacaaacggc ctatgttgcgtt atggttggaa
 2381 ggggggggg gtcgttttttgcgtt gtcgcacca aacaaacggc ctatgttgcgtt atggttggaa
 2451 ttcgttttttgcgtt gtcgcacca aacaaacggc ctatgttgcgtt atggttggaa
 2521 gtcgttttttgcgtt gtcgcacca aacaaacggc ctatgttgcgtt atggttggaa
 2591 cgcggactg cccggacac gtcgttttttgcgtt gtcgcacca aacaaacggc ctatgttgcgtt atggttggaa
 2661 acacagttccca aaaaatggc agtactgttgcgtt ttgcgttgcgtt

Figure 9

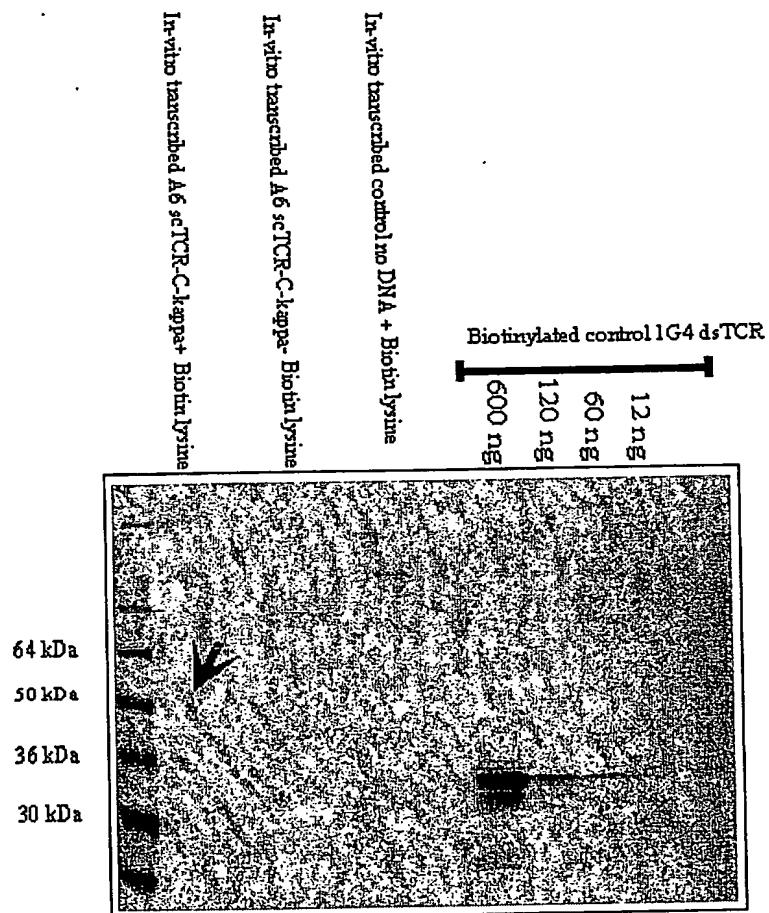
A6.scTCR-C-kappa cloned into pUC19-T7

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51 gagggagcca ttgcctctc caactgcact tacagtgacc gaggttccca
101 gtccttcc tggtaacagac aatattctgg gaaaaggcct gagggtataa
151 tgtccatata ctccaaatggt gacaaaagaag atggaaagggt tacagcacag
201 ctcataaaag ccagccagta tggttctctg ctcatcagag actcccaagcc
251 cagtgattca gccacctacc tctgtgcccgt tacaactgac agctggggga
301 aattgcagtt tggagcaggg acccaggtt tggtcaccgg tggaggccgt
351 tcaggccggag gtggatccgg cgggtggccgg tcgaacggctg gtgtcactca
401 gacccaaaaa ttccaggtcc tgaagacagg acagagcatg acactgcagt
451 gtgccccagga tatgaaccat gaatacatgt cctggtatcg acaagaccca
501 ggcattgggc tgaggctgtat tcattactca gttgggtgtcg gtatcactga
551 ccaaggagaa gtccccaatgt gctacaatgt ctccagatca accacagagg
601 atttcccgct caggctgtcg tggctgtc cttcccaagac atctgtgtac
651 ttctgtgcca gcaggccggg actagccggg gggcgtaccagg agcagtactt
701 cggccgggc accaggctca cggtcacaga ggacctgaaa aacgtgttcc
751 caccggagggt cgctgtgtt gagccatcg aagcagagat ctcccacacc
801 caaaaggcca cactgggtgtg cttggccaca ggcttctacc ccgaccacgt
851 ggagctgagc tgggggtga atgggaagga ggtgcacagt ggggtcagca
901 cagaccggca gccccctcaag gaggcagcccg ccctcaatga ctccagatac
951 gctctgagca gcccgtcgag ggtctcgccc accttctggc aggacccccc
1001 caaccacttc cgctgtcaag tccagtctca cgggtctcg gagaatgacg
1051 agtggaccca ggataggccc aaacccgtca cccagatcg cagcggccgag
1101 gcctggggta gaggcagacgg tggaggccgt tcactcagca gcaccctgac
1151 gctgagccaa gcaactacg agaaacacaa agtctacgccc tgcgaagtca
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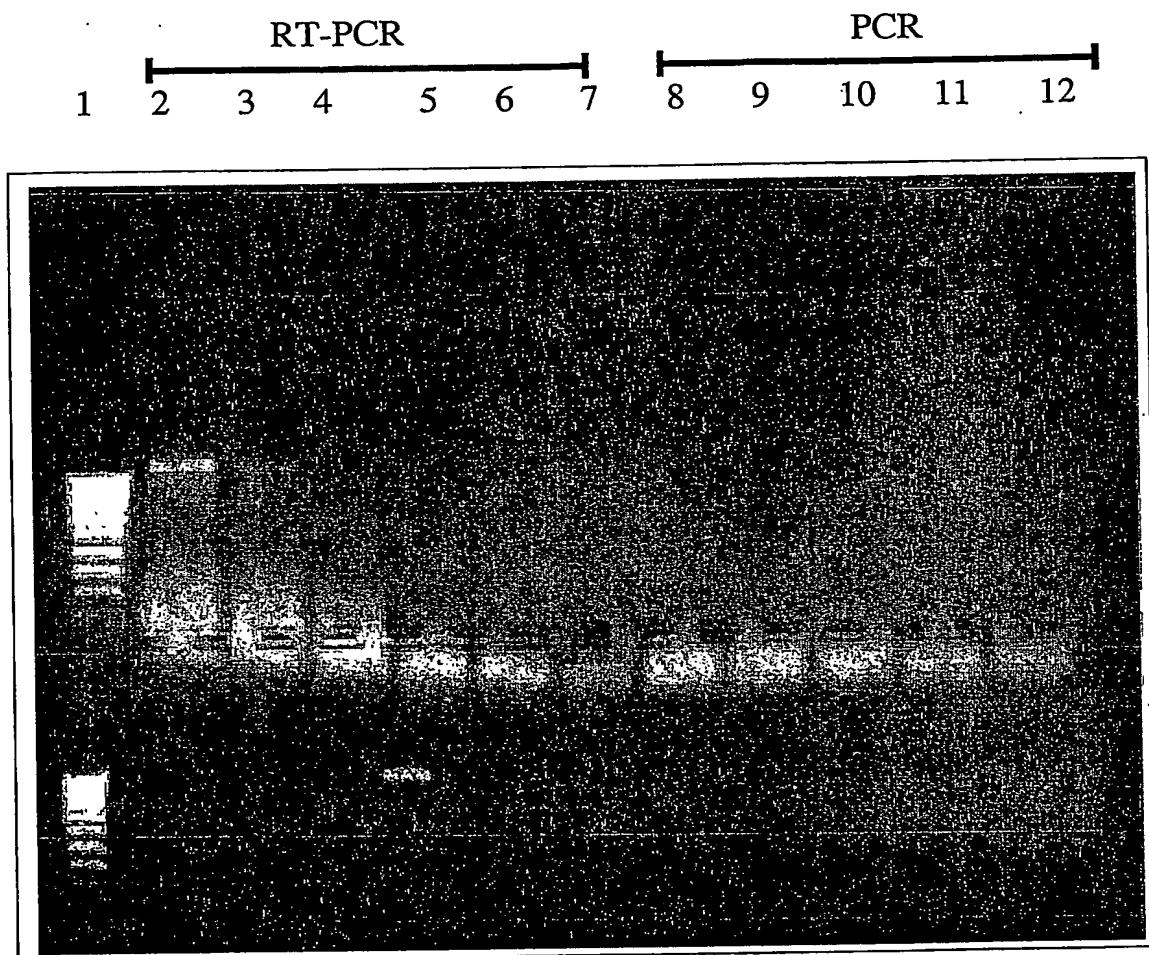
```

Figure 10



The A6 scTCR-C-Kappa protein is shown in the above western blot with an arrow.

Figure 11



13 14 15

Lane 1 Bioline 100bp DNA marker

Lane 2 A6scTCR-C-Kappa reaction selected against HLA-A2 TAX beads

Lane 3 A6scTCR-C-Kappa reaction selected against HLA-A2 TAX beads in the presence of 10 microgrammes of soluble A6scTCR

Lane 4 A6scTCR-C-Kappa reaction selected against control beads

Lane 5 Control no DNA reaction selected against HLA-A2-TAX beads

Lane 6 Control no DNA reaction selected against HLA-A2 TAX beads in the presence of 10 microgrammes of soluble A6scTCR

Lane 7 Control no DNA reaction selected against control beads

Lanes 8-12 and lane 13 are as lanes 2-7 except no reverse transcriptase was added just Roche high fidelity taq. These are the DNA contamination controls.

Lane 13 RT-PCR positive control.

Figure 12a (Clone 9)

Clone 9 Mutated A6 TCR β chain DNA sequence

```
gctgggtcaactcagacccaaaattccaggccttgaagacaggacagagcatgacactgcagtgtgccaggatataaccat  
gaatacatgtcctggtatcgacaagacccaggcatgggctgaggctgattcattactcagttggctgttatcactgaccaagga  
gaagtccccaatggctacaatgtctccagatcaaccacagaggattcccgctcaggctgtcggctgtccctccagacatct  
gtgtactctgtgccaggcaggccggactagcgggagggtgaccagagcagttacttcggccggcaccaggctacggtcac  
agaggacactgaaaaacgtgttccacccgaggctgtgtttgagccatcagaacgagcagatctccacacccaaaaggcca  
cactggtgtgcctggccacaggcttctaccccgaccacgtggagctgagctgggtgaatggaaaggagggtgcacagtgggg  
tctgcacagaccccgagccctcaaggaggcagccgcctcaatgactccagatacgttgcagcagccgcctgagggtctcg  
ccaccctctggcaggaccccaaccacttccgctgtcaagtccagttctacggctctggagaatgacgagtggacccagga  
tagggccaaacccgtcaccaggatcgtcagcggcggctgggttagagcagac
```

Figure 12b (Clone 9)

Clone 9 Mutated A6 TCR β chain amino acid sequence

```
Agvtqtpkfqvltkqsmtlqcaqdmnheymswyrqdpgmglrlihysvgagitdqgevpngynvsrsttedfpirlsaapsqts  
vyfcasrplagg*peqyfgptrltvtedlknvfppevavfepseaeishtqkatlvclatgfypdhvelswvngkevhsgvctd  
pqplkeqpalndsryalssrlvsatfwqdprnhfrcqvfylsendewtqdrakpvtqivsaeawgrad
```

* - Denotes the position of the amino acid corresponding to the introduced 'opal' stop codon, this will generally result in the substitution of a tryptophan (w) residue into the TCR β chain at this point.

Figure 13 (Clone 49)

Clone 49 Mutated A6 TCR β chain DNA sequence

```
gctgggtcaactcagacccaaaattccagggtccatgaaagacaggacagagcatgacactgttagtgtgcccaggatataaccat
gaatacatgtccctggatcgacaaggacccaggcatggggctgaggctgattactcagttgggtctggatcactgaccaaggg
gaagtccccatggctacaatgtctccagatcaaccacagaggattttccctgtcaggctgtcggtgtctccctccagacatct
gtgtacttctgtgccagcaggccggactagcgggagggcgaccagagcagacttcgggccccaccaggctacggcacggtcac
agaggacactgaaaaacgtgttcccaccccgagggtcgctgttgttagccatcagaaggcagagatctccacacccaaaaggcca
caactgggtgtgcctggccacaggcttaccccgaccacgtggagctgagctgggtgtaaatggaaaggagggtgcacagtgggg
tctgcacagaccccgcaagccctcaaggagcagccgcctcaatgactccagatacgtctgagcagccgcctgagggtctcg
ccacccctgtccaggaccccgcaaccactccgtcaagtccagtttacggctctcgagaaatgacgagtggacccagac
tagggccaaaccgtcacccagatcgtaagcgccgaggctgggttagagcagac
```

Figure 14a (Clone 134)

Clone 134 Mutated A6 TCR β chain DNA sequence

gctgggtcactcagacccaaaattccaggctctaagacaggacagacatgacactgcagtgtgcccccaggatataaccat
gaatacatgtcctggatcgacaagaccccaggcatggggctgaggctgattcattactcagttgtctgttatcactgaccaagga
gaagtccccatggctacaatgtctccagatcaaccacagaggattcccgctcaggctgtctcggtctgtccctccacacatct
gtgtacttctgtcctcgaggccgggctgtatgagtgcggaaaccagagcagacttcggccgggcaccaggctacggtcac
agaggactgaaaaacgtgttccaccggaggctcgctgtttgagccatcagaaggcagagatctccacacccaaaaggcca
cactgggtgcctggccaccggtttctacccgaccacgtggagctgagctgggtggtaatgggaaggagggtgcacagtgggt
ctgcacagaccccgccagccctcaaggagcagccgcctcaatgactccagatacgctctgagcagccgcgtgagggtctcg
ccacccctctggcaggaccggcccaaccacttccgctgtcaagtccagttcacgggcctctggagaatgacgagtggaccagg
tagggccaaacccgtcaccaggatcgtcagcggccgaggcctgggttagagcagactaagcttgaattc

Figure 14b (Clone 134)

Clone 134A Mutated A6 TCR β chain amino acid sequence (BIAcore)

mnagvtqtpkfqvlktgqsmtlqcaqdmnheymswyrqdpqmgmlrihysvgagitdqgevpngynvsrsttedfplrlsaaps
qtsvyfcasrpglmsaapeeqyfgpgrtrtvedlknvfppeavfepseaeishtqkatlvclatgfypdhvelswvngkevhsg
vctdpqplkeqpalndsryalssrlvsatfwqdprnhfrcqvfqyglsendewtqdrakpvtqivsaeawgrad*

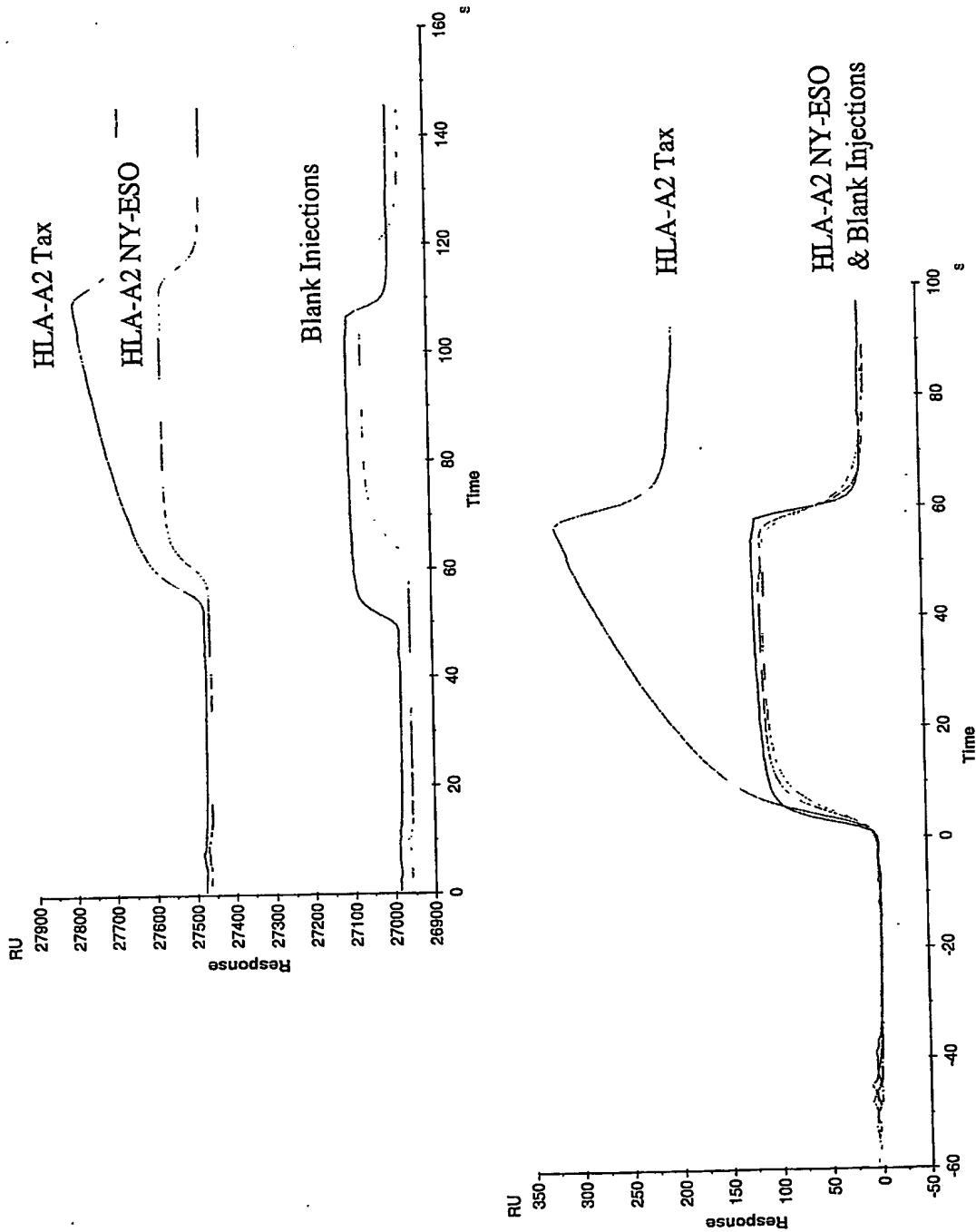
Figure 14c (Clone 134)

Clone 134 Mutated A6 TCR β chain amino acid sequence (ELISA)

agvtqtpkfqvlktgqsmtlqcaqdmnheymswyrqdpqmgmlrihysvgagitdqgevpngynvsrsttedfplrlsaapsqts
vycasrpglmsaapeeqyfgpgrtrtvedlknvfppeavfepseaeishtqkatlvclatgfypdhvelswvngkevhsgvct
dpqplkeqpalndsryalssrlvsatfwqdprnhfrcqvfqyglsendewtqdrakpvtqivsaeawgrad

18/34
Figure 15

A6 TCR clone 134



19/34
Figure 16

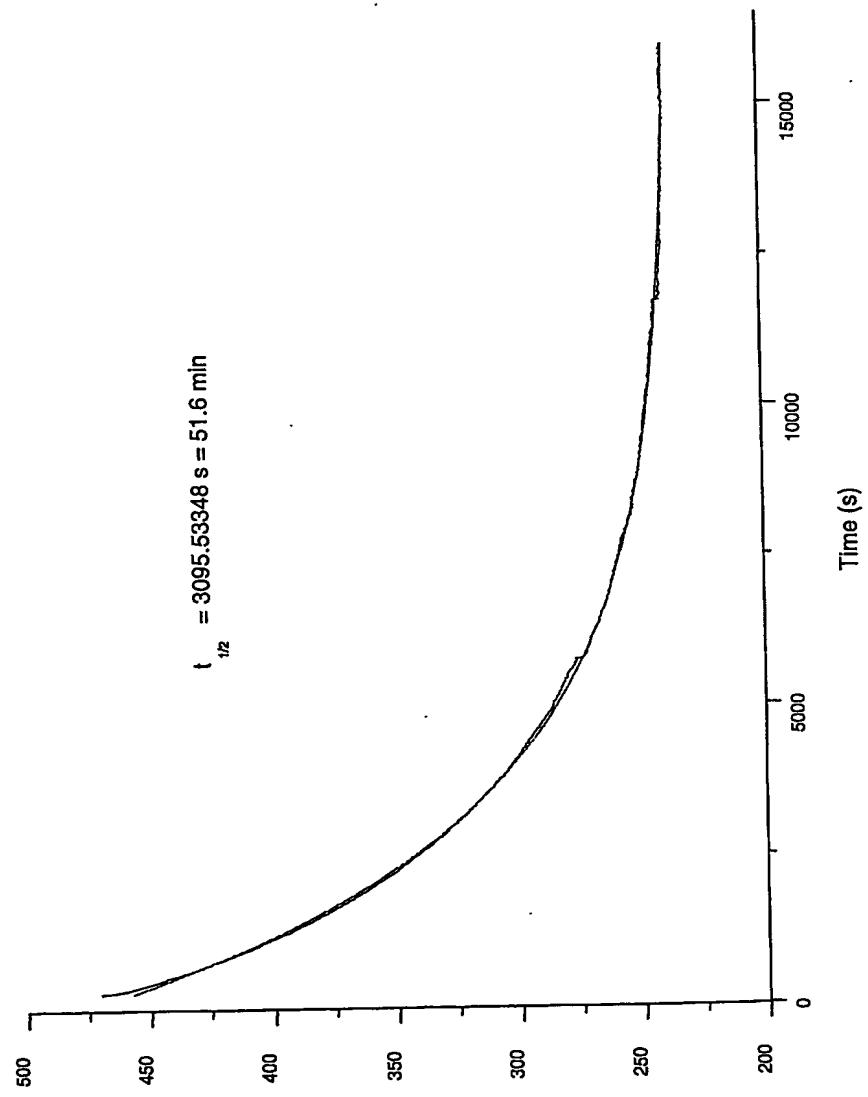


Figure 17a

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 ggcgtattacaacacctccagtggtttaggcaggaccctgggaaagggtcacatctgttgcttattcagtcagtcagaga
 gagcaaaacaagtggaaagacttaatgcctcgctggataaattcatcaggacgttagtactttatacattgcagcttcagcctgg
 tgactcagccacaccttctgtgctgtgaggccacatcaggaggaagctacataccatatttggaaagaggaaccaggcct
 tattgttcatccgtatattccagaaccctgaccctgcccgttaccagctgagagactctaaatccagtgacaagtctgtgcct
 attcaccgatttgattctcaaacaatgtgtcacaaggattctgtatcagatgtgtatcagacaaatgtgtctgtagacatg
 aggtctatggacttcaagagcaacagtgcgtggcctggagcaacaaatctgacttgcattgtgcaaaacgcctcaacaaca
 gcattattccagaagacaccccttccccagccagaaagtccctaa

Figure 17b

atgggtgtactcagacccaaaattccaggtcctgaagacaggacagcatgacactgcagtgtgcccaggatata
 ccatgaatacatgtcctggatcgacaagaccaggcatgggctgaggctgattactcagttggctggatctactg
 accaaggagaagtcccaatggctacaatgtccagatcaaccacagaggattcccgctcaggctgtcggctgctc
 cctccagacatctgttactctgtgcccagtgatctgtgggaaacacccggggagctgttttgagaaggcttaggctg
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 caaaaggccacactgggtgtgcctggccacaggcttctacccgaccacgtggagctgagctgggtgaatgggagg
 aggtgcacagtgggtctgcacagacccgcagccctcaaggagcagccgcctcaatgactccagatacgctctgag
 cagccgcctgagggctcgccacccctgtggcaggaccccgcaaccactccgctgtcaagtccagttctacggctctc
 ggagaatgacgagtgccaggataggccaaacccgtcacccagatgtcagcgcgaggcctgggttagagcag
 actaa

Figure 18a

M Q E X T Q I P A A L S V P E G E N L V L N C S F T D S A I Y N L Q W F R Q
 D P G K G L T S L L I Q S S Q R E Q T S G R L N A S L D K S S G R S T L Y I
 A A S Q P G D S A T Y L C A V R P T S G G S Y I P T F G R G T S L I V H P Y I
 Q N P D P A V Y Q L R D S K S S D K S V C L F T D F D S Q T N V S Q S K D S
 D V Y I T D K C V L D M R S M D F K S N S A V A W S N K S D F A C A N A F
 N N S I I P E D T F F P S P E S S Stop

Figure 18b

M G V T Q T P K F Q V L K T G Q S M T L Q C A Q D M N H E Y M S W Y R Q
 D P G Met G L R L I H Y S V G A G I T D Q G E V P N G Y N V S R S T T E D F
 P L R L L S A A P S Q T S V Y F C A S S Y V G N T G E L F F G E G S R L T V L
 E D L K N V F P P E V A V F E P S E A E I S H T Q K A T L V C L A T G F Y P D
 H V E L S W W V N G K E V H S G V C T D P Q P L K E Q P A L N D S R Y A L
 S S R L R V S A T F W Q D P R N H F R C Q V Q F Y G L S E N D E W T Q D R
 A K P V T Q I V S A E A W G R A D Stop

Figure 19

1 TTCCCTGGCCT TTTGCTGGCC TTTTGCTCAC ATGTAATGTC AGTTAGCTCA
 51 AAGGACCGGA AAACGACCGG AAAACGAGTG TACATTACAC TCAATCGAGT
 101 CTCATTAGGC ACCCCAGGCT TTACACTTTA TGCTTCCGGC TCGTATGTTG
 151 GAGTAATCCG TGGGGTCCGA AATGTGAAAT ACGAAGGCGG AGCATAAC
 201 TGTTGAATTG TGACGGGATA ACAATTTCAC ACAGGAAACA GCTATGACCA
 251 ACACCTTAAC ACTCGCTAT TGTTAAAGTG TGCTCTTTGT CGATACTGGT
 301 TGATTACGCC AAGCTACGTA CTTAAGTATT CTATTTCAAG GAGACAGTC
 351 ACTAATGCCG TTCGATGCCAT GAATTCAAA GATAAAAGITC CTCTGTCAGT
 401 K Y L L P T A A A G L L L A
 451 TAATGAAATA CCTATTGCT ACGGCAGGCC CTGGATTGTT ATTACTCGCG
 501 ATTACTTTAT GGATAACGGA TGCCGTCGGC GACCTAACAA TAATGAGCGC
 551 NcoI
 601 PstI
 651 -----
 701 -----
 751 -----
 801 -----
 851 -----
 901 -----
 951 -----
 1001 -----
 1051 -----
 1101 -----
 A Q P A M A K Q E V T Q I P A A L
 251 CCCAGCCGG CCATGGCAA ACAGGAGGTG ACGCAGATTC CTGCAGCTCT
 301 CGGGTCGGCC GGTACCGGTT TGCTCTCCAC TGCGTCTAAG GACGTCGAGA
 351 PstI
 401 -----
 451 -----
 501 -----
 551 -----
 601 -----
 651 -----
 701 -----
 751 -----
 801 -----
 851 -----
 901 -----
 951 -----
 1001 -----
 1051 -----
 1101 -----
 S V P E G E N L V L N C S F T D S
 301 GAGTGTCCA GAAGGAGAAA ACTTGGTTCT CAACTGCAGT TTCACTGATA
 351 CTCACAGGGT CTTCTCTTT TGAAACCAAGA GTTGACGTCA AAGTGAATAT
 401 A I Y N L Q W F R Q D P G K G L
 451 GCGCTATTTA CAACCTCCAG TGTTTAGGC AGGACCTGG GAAAGGTC
 501 CGCGATAAT GTTGGAGGTG ACCAAATCCG TCCTGGGACC CTTCAGAG
 551 T S L L L I Q S S Q R E Q T S G R
 601 ACATCTCTGT TGCTTATTCA GTCAAGTCAG AGAGAGCAA CAAGTGGAG
 651 TGTTAGAGACA ACGAATAAGT CAGTTCACTGC TCTCTCGTTT GTTCACCTTC
 701 ACTTAATGCC TCGCTGGATA AATCATCAGG ACCTAGTACT TTATACATG
 751 TGAATTACGG AGCAGACCTAT TTAGTAGTCC TGCACTATGA AATATGTAAC
 801 A S Q P G D S A T Y L C A V R P
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 901 GTCGAAGACT CGGACCACTG AGCTGGTGGA TGGAGACAG ACACTCCGGG
 951 T S G G S Y I P T F G R G T S L I
 1001 T S G G S Y I P T F G R G T S L I
 1051 ACATCAGGAG GAAGCTACAT ACCTACATTG GGAAGAGGAA CCAGCTTAT
 1101 TGTAGTCCTC CTTCGATGTA TGGATGTTAA CCTTCTCCCT GGTCGGAATA
 BamHI

 V H P Y I Q N P D P A V Y Q L R D
 601 TGTTCATCCG TATATCCAGA ACCCGGATCC TGCGTGTAC CAGCTGAGAG
 651 ACAAGTAGGC ATATAGGTCT TGGCCTAGG ACGGCACATG GTCGACTCTC
 701 S K S S D K S V C L F T D F D S
 751 ACTCTAAATC CAGTGACAAG TCTGTCTGCC TATTCAACCGA TTTTGATTCT
 801 TGAGATTAG GTCACTGTT AGACAGACGG ATAAGTGGCT AAAACTAAGA
 851 Q T N V S Q S K D S D V Y I T D K
 901 CAAACAAATG TGTCACAAAG TAAGGATTCT GATGTGTATA TCACAGACAA
 951 GTTTGTTTAC ACAGTGTTC ATTCTTAAGA CTACACATAT AGTGTCTGTT
 1001 C V L D M R S M D F K S N S A V A
 1051 ATGTGTGCTA GACATGAGGT CTATGGACTT CAAGAGCAAC AGTGTGTGG
 1101 TACACACGAT CTGTACTCCA GATACTGAA GTTCTCGTTC TCACGACACC
 W S N K S D F A C A N A F N N S
 CCTGGAGCAA CAAATCTGAC TTTGCATGTG CAAACGCCCT CAACAAACAGC
 GGACCTCGTT GTTGTGACTG AACGTACAC GTTGTGCGAA GTTGTGTGCG
 PstI
 AvrII

 I I P E D T F F P S P E S S * *
 851 ATTATTCAG AAGACACCTT CTTCCCCAGC CCAGAAAGTT CCTAATAACC
 TAATAAGGTC TTCTGTGGAA GAAGGGTCG GGTCTTCAA GGATTATTGG
 AvrII EcorI

 M K K L
 901 TAGGTAAATT AAGAATTCTT TAAGAAGGG ATATACATAT GAAAAATAA
 ATCCAATTAA TTCTTAAGAA ATTCTTCCC TATATGTATA CTTTTTTAA
 BssHII

 L F A I P L V V P F Y S H S A Q A
 951 TTATTGCAGA TTCTTTAGT TGTCCTTTC TATTCTCACCA GCGCGCAGGC
 AATAAGCGT AAGGAATCA ACAAGGAAAG ATAAGAGTGT CGCGCGTCCG
 G V T Q T P K F Q V L K T G Q S M
 1001 TGGTGTCACT CAGACCCAA AATTCCAGGT CCTGAAGACA GGACAGAGCA
 ACCACAGTGA GTCTGGGTT TTAAGGTCCA GGACTTCTGT CCTGTCCTG
 PstI

 T L Q C A Q D M N H E Y M S W Y
 1051 TGACACTGCA GTGCCCCAG GATATGAACC ATGAATACAT GTCCCTGGTAT
 ACTGTGACGT CACACGGTC CTATACCTGG TACTTATGTA CAGGACCAT
 R Q D P G M G L R L I H Y S V G A
 1101 CGACAAGACC CAGGCATGGG GCTGAGGCTG ATTCAATTACT CAGTGGTGC

GCTGTTCTGG GTCCCTACCC CGACTCCGAC TAAGTAATGA GTCAACCACG
 1151 . G I T D Q G E V P N G Y N V S R S
 TGGTATCACT GACCAAGGAG AAGTCCCCAA TGGCTACAAAT GTCTCCAGAT
 ACCATAGTGA CTGGTTCCTC TTCAAGGGGTT ACCGATGTAA CAGAGGTCTA
 . T T E D F P L R L L S A A P S Q
 1201 CAACACAGA GGATTTCCCG CTCAGGCTGC TGTGGCTGC TCCCTCCAG
 GTTGGTGTCT CCTAAAGGGC GAGTCCGACG ACAGCCGACG AGGGAGGGC
 T S V Y F C A S S Y V G N T G E L
 1251 ACATCTGTGT ACTTCTGTGC CAGCAGTTAC GTCGGGAAACA CCGGGGAGCT
 TGTAGACACA TGAAGACACG GTCTCAATG CAGCCCTGT GGCCCTCGA
 . F F G E G S R L T V L E D L K N V
 1301 GTTGGTGGAA GAAGGCTCTA GGCTGACCGT ACTGGAGGAC CTGAAAAACG
 CAAAAAACCT CTTCCGAGAT CCGACTGGCA TGACCTCCCTG GACTTTTGC
 AvaI BgIII

 . F P P E V A V F E P S E A E I S
 1351 TGTTCCACCGAGGAGCTGCT GTGTTGAGC CATCAGAACG AGAGATCTCC
 ACAAGGGTGG GCTCAGCGA CACAAACTCG GTACTCTTCG TCTCTAGAGG
 1401 H T Q K A T L V C L A T G F Y P D
 CACACCCAAA AGGCCACACT GGTTGTGCTG GCCACAGGCT TCTACCCGA
 GTGTGGTTT TCCGGTGTGA CCACACGGAC CGGTGTCCGA AGATGGGCT
 ApaLI

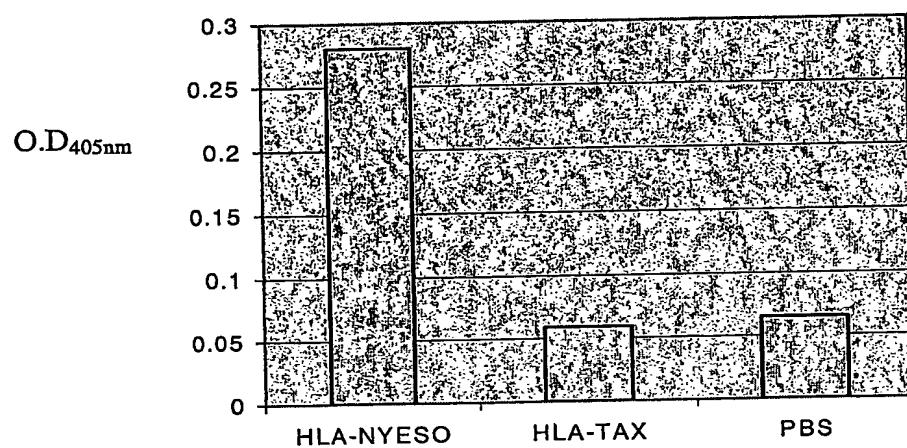
 . H V E L S W W V N G K E V H S G V
 1451 CCACGTGGAG CTGAGCTGGT GGGTGAATGG GAAGGGAGGTG CACAGTGGGG
 GGTGCACCTC GACTCGACCA CCCACTTAC CTTCCCTCCAC GTGTCAACCC
 . C T D P Q P L K E Q P A L N D S
 1501 TCTGCACAGA CCCGCAGCCCC CTCAGGAGC AGCCCGCCCT CAATGACTCC
 AGACGTGTCT GGGCGTGGG GAGTTCTCG TCGGGCGGGA GTTACTGAGG
 R Y A L S S R L R V S A T F W Q D
 1551 AGATACGCTC TGAGCAGCCG CCTGAGGGTC TCGGCCACCT TCTGGCAGGA
 TCTATGCGAG ACTCGTCGGC GGACTCCAG AGCCGGTGGAGACCGTCCT
 . P R N H F R C Q V Q F Y G L S E N
 1601 CCCCGCAAC CACTCCGCT GTCAAGTCCA GTTCTACGGG CTCTCGGAGA
 GGGGGCGTTG GTGAAGGCGA CAGTTCAAGGT CAAGATGCC GAGAGCCTCT
 . D E W T Q D R A K P V T Q I V S
 1651 ATGACGAGTG GACCCAGGAT AGGGCCAAAC CCGTCACCCA GATCGTCAGC
 TACTGCTCAC CTGGGTCTA TCCCGGTTG GGCAGTGGGT CTAGCAGTCG
 XbaI

 NotI

 1701 A E A W G R A D A A A
 GCCGAGGCCT GGGGTAGAGC AGACGCGGCC GCA
 1702 CGGCTCCGGA CCCCATCTCG TCTGCGCCGG CGT

23/34

Figure 20



24/34

Figure 21

DRA0101

1 ggatccatgg ccataagtgg agtccctgtg ctaggatttt tcatcatagc tgtgctgatg~
61 agcgctcagg aatcatgggc tatcaaagaa gaacatgtga tcatccaggc cgagtttat~
121 ctgaatccctg accaatcagg cgagtttatg tttgactttg atggatgtga gattttccat~
181 gtggatatgg caaagaagga gacggctctgg cggcttgaag aatttggacg atttggcagc~
241 tttgaggctc aagggtgcatt ggccaaacata gctgtggaca aagccaaacct gggaaatcatg~
301 acaaagcgct ccaactatac tccgatcacc aatgtacctc cagaggttaac tgtgctcacg~
361 aacagccctg tggaaacttag agagcccaac gtcctcatct gtttcatcga caagttcacc~
421 ccaccagttt tcaatgtcac gtggcttcga aatggaaaac ctgtcaccac aggagtgtca~
481 gagacagttt tcctgcccag ggaagaccac cttttccgca agttccacta tctcccttc~
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721 ggggttcagaatccaaatggc caatctactg aadagaaagg aaaaacttgcgatgttcatccctg~
781 gcaatggatgg gatctggatgg tggatgttgc aatgttgg aagatgttgc aatgttgc aatgttgc~
841 catgagtagg atcc

XXX

Fos Leucine zipper codons
Biotinylation tag codons

Figure 22

28/34

10021 cttccggctc gtatgttgc tggaaattgtg agcggataac aatttcacac aggaaacacg
10081 tatgaccatg attacg



- Restriction enzyme sites

Figure 23

1 ggtaccggat ccagcatggt gtgtctgaag cttccctggag gtcctgcac gacagcgctg
61 acagtgcacac tgatgggtct gagctccccca ctggctttgt ccggagacac cggacctaag
121 tagctcaagc agaacacact gaaactggct tccgggtggcg gatctctagt tccacgcggt
181 agtggaggcg gtgggtccgg agacacgcgt ccacgtttct ttgtggcagct taagtttcaa
241 tgcgtatcc tcaatgggac ggagcgggtg cgggtgctgg aaagatgcac ctataaccaa
301 gaggagtccg tgcgcattcga cagcgcacgt ggggagttacc gggcggtgac ggagctgggg
361 cggcctgtatg ccgagttactg gaacagccag aaggaccttc tggagcagag gcccggccgg
421 gtggacaccc tactgcagaca caactacggg gttggtgaga gtcctcacagt gcagcggcga
481 gttgagccta aggtgactgt gtatccctca aagaccccagc ccctgcagca ccacaaaccc
541 ctggctgtct ctgtgagtgg ttttatcca ggcgcattt aagtgcaggta gttccggaaac
601 ggcgcaggaa agaaggctgg ggtgggttcc acaggcctgt atcggaaatgg agattggacc
661 ttccagaccc tggtgatgt gaaacagtt cctcggagtg gagaggttta cacctgcca
721 gtggagcacc caagtgtgac gagccctctc acagtggaaat ggagagcacg gtctgaatct
781 gcacacagca aggtgcacgg aggccgggg ggttagaaatcg Cccggctggatggatggatgg
841 aaaaacccgtga aagctcagaa ctccggagctg gcaatcccccggcccaacatgtt cggggaaacag
901 ctgcgcacagc taaaacagaa aggtgtgaaat ctttaggatc c

- Jun Leucine zipper codons
- HLA-loaded peptide

30/34

Figure 24

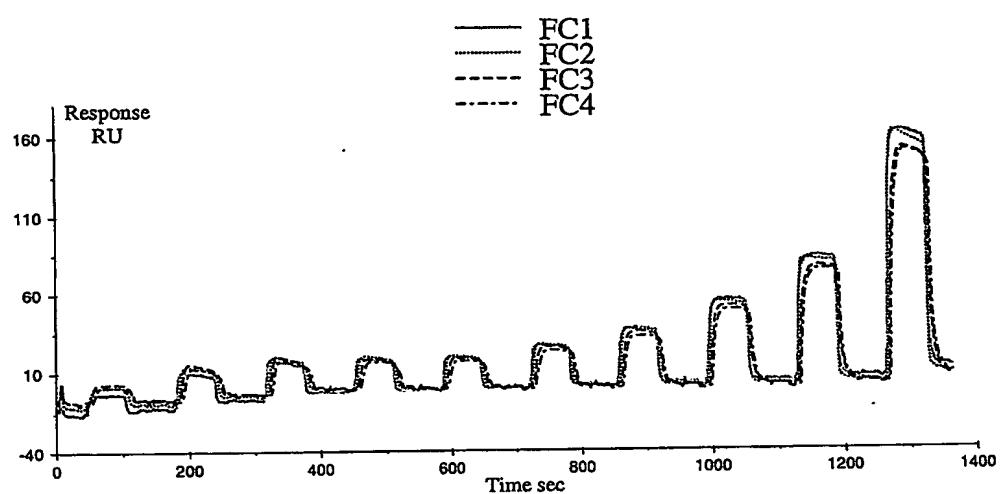
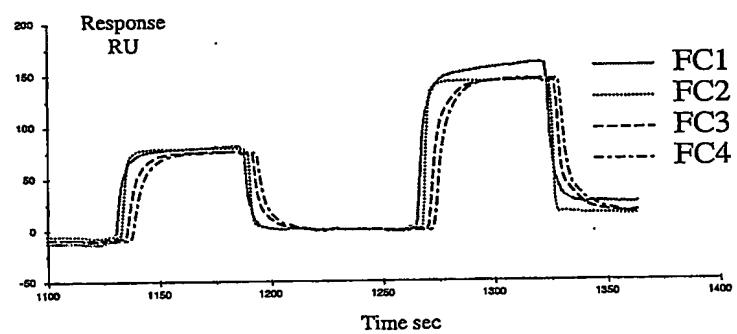


Figure 25



32/34

Figure 26

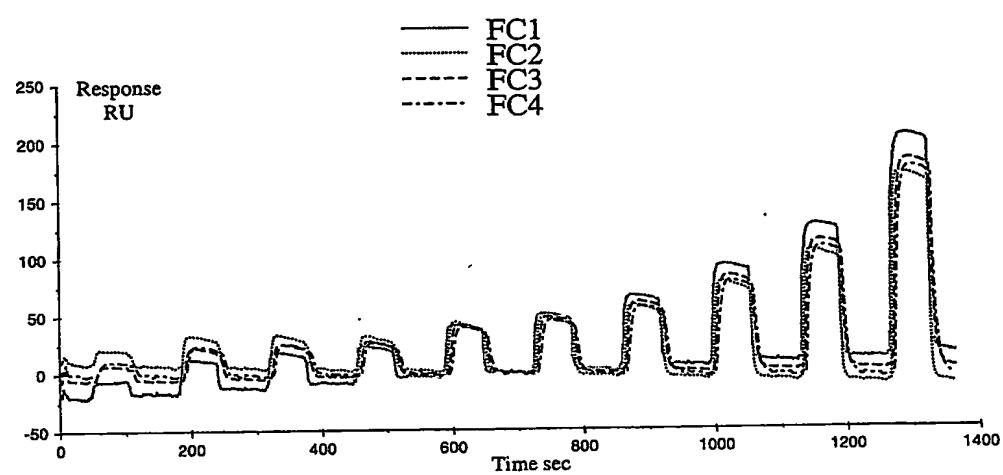
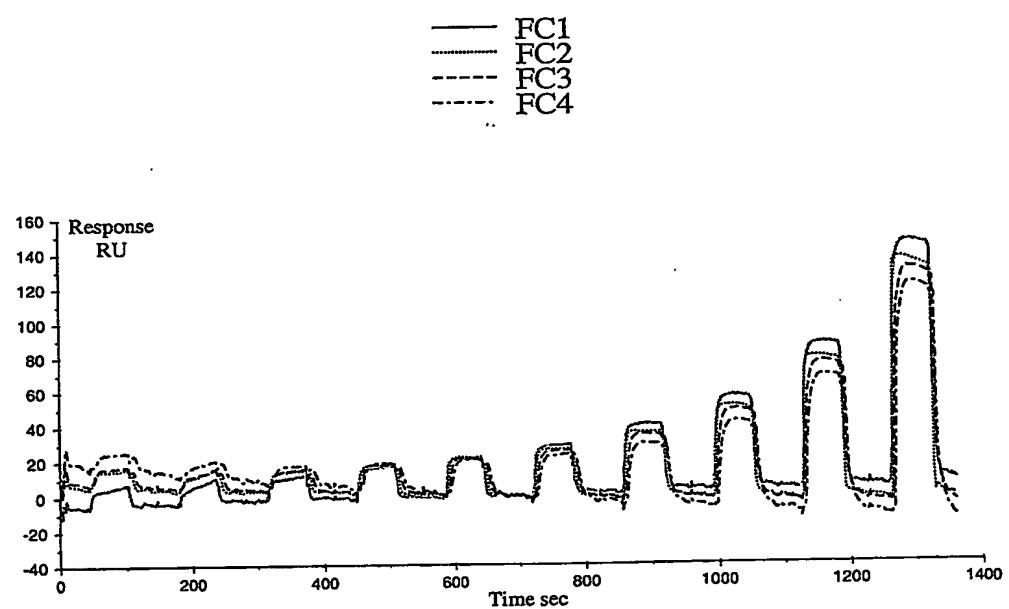
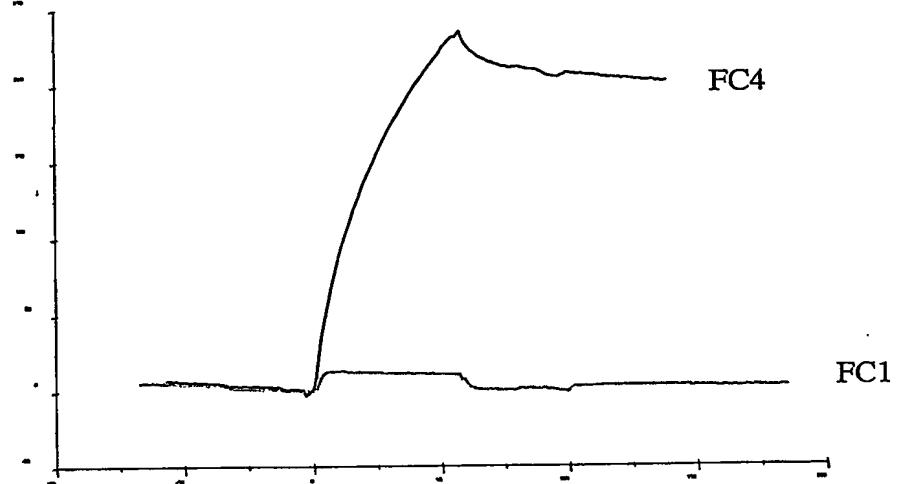


Figure 27



34/34

Figure 28





PCT Application

GB0304636

